



PA (TUFT ) TUFTS COLLEGE.  
 XX  
 PI Levy SB, McMurry LM;  
 XX  
 DR WPI: 1999-458702/38.  
 DR N-PSDB: AAX88348.  
 XX  
 PT Identifying antimicrobials that target enoyl acyl carrier protein  
 PT reductase, for therapeutic use and for incorporation into e.g. soaps  
 PT and detergents  
 XX  
 PS Claim 77, Fig 2: 80pp: English.  
 XX  
 CC This invention describes a novel method for identifying antimicrobials  
 CC (1) that interact with an enoyl acyl carrier protein (ACP) reductase  
 CC (E) polypeptide, which is essential for fatty acid biosynthesis, by  
 CC contacting ER with test compound and detecting any interaction. The  
 CC identified antimicrobials have antibacterial, antifungal, antiprotocozal,  
 CC antiparasitic and antiviral activity. The products of the invention are  
 CC used (1) therapeutically to treat a wide variety of viral, bacterial,  
 CC fungal, yeast and protozoal infections, in both humans and animals, and  
 CC (11) in disinfectants, detergents, soaps, mouthwashes, toothpastes and  
 CC also contraceptive devices. The invention describes methods for (1)  
 CC identifying a (1) from its effect on enzymatic activity of ER, (2)  
 CC identifying a (1) from its ability to inhibit fatty acid biosynthesis in  
 CC a microbe, (3) identifying a (1) that interacts with a mutant ER, (4)  
 CC identifying (1) that inhibit proliferation or viability of a microbe that  
 CC is resistant to triclosan or to NSAM (non-specific antimicrobials). This  
 CC sequence represents a mutant Escherichia coli FabI protein which  
 CC interacts with the enoyl-acyl carrier protein (ACP) reductase to  
 CC illustrate the method of the invention.  
 XX  
 SQ Sequence 262 AA;  
 Query Match 62.8%; Score 49; DB 20; Length 262;  
 Best Local Similarity 60.0%; Pred. No. 2.2;  
 Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MRYRASALGSDGVRV 15  
 Db 170 VRYMANMGPESGVRV 184  
 RESULT 2  
 AAU34559  
 ID AU34559 standard; Protein: 262 AA.  
 AC AU34559;  
 XX  
 DT 14-FEB-2002 (first entry)  
 XX  
 DE E. coli cellular proliferation protein #140.  
 XX  
 KW Antisense; prokaryotic cellular proliferation protein;  
 KW antibiotic; antibacterial; drug design.  
 XX  
 OS Escherichia coli.  
 XX  
 PN WO200170955-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 21-MAR-2001; 2001WO-US09180.  
 XX  
 PR 21-MAR-2000; 2000US-191078P.  
 PR 23-MAY-2000; 2000US-206848P.  
 PR 26-MAY-2000; 2000US-207727P.  
 PR 23-OCT-2000; 2000US-242578P.  
 PR 27-NOV-2000; 2000US-253625P.  
 PR 22-DEC-2000; 2000US-257931P.  
 PR 16-FEB-2001; 2001US-269308P.  
 XX  
 PA (ELIT-) ELITRA PHARM INC.

XX  
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;  
 PI Yamamoto RT, Xu HH;  
 XX  
 DR WPI: 2001-611495/70.  
 DR N-PSDB: AAS52418.  
 XX  
 PT New polynucleotides for the identification and development of  
 PT antibiotics, comprise sequences of antisense nucleic acids -  
 XX  
 PS Example 3; Seq ID No 10152; 511pp: English.  
 XX  
 CC The invention relates to antisense inhibitors of genes essential to  
 CC prokaryotic cellular proliferation, their use in identifying the  
 CC genes, their use in the discovery of novel antibiotics, the essential  
 CC genes themselves and the encoded proteins. The prokaryotes used are  
 CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella  
 CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The  
 CC invention is also useful for the identification of potential new targets  
 CC for antibiotic development. The antisense nucleic acids can also be used  
 CC to identify proteins used in proliferation, to express these proteins,  
 CC and to obtain antibodies capable of binding to the expressed proteins.  
 CC The proteins can be used to screen compounds in rational drug discovery  
 CC programmes. The antisense nucleic acid sequence is also useful to screen  
 CC for homologous nucleic acids which are required for cell proliferation in  
 CC a wide variety of organisms. The present sequence represents an  
 CC essential prokaryotic cellular proliferation protein.  
 CC Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 262 AA;  
 Query Match 62.8%; Score 49; DB 22; Length 262;  
 Best Local Similarity 60.0%; Pred. No. 2.2;  
 Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MRYRASALGSDGVRV 15  
 Db 170 VRYMANMGPESGVRV 184  
 RESULT 3  
 AAE02203  
 ID AAE02203 standard; Protein: 262 AA.  
 AC AAE02203;  
 XX  
 DT 31-JUL-2001 (first entry)  
 XX  
 DE Escherichia coli NADPH-dependent enoyl-ACP reductase (FabI).  
 XX  
 KW FabI; high throughput method; fatty acid biosynthesis; therapy;  
 KW bacterial enzyme; biological agent screening; otitis media; empyema;  
 KW bacterial tracheitis; acute epiglottitis; thyroditis; lung abscess;  
 KW infective endocarditis; secretory diarrhoea; splenic; retroperitoneal;  
 KW intrarenal; perinephric; cutaneous; abscess; blepharitis;  
 KW conjunctivitis; keratitis; endophthalmitis; presepal; orbital;  
 KW cellulitis; dacryocystitis; epididymitis; abscess; toxic shock syndrome;  
 KW impetigo; folliculitis; wound infection; bacterial myositis;  
 KW septic arthritis; osteomyelitis; enoyl-ACP reductase;  
 KW acyl carrier protein.  
 XX  
 OS Escherichia coli.  
 XX  
 PN WO200130988-A1.  
 XX  
 PD 03-MAY-2001.  
 XX  
 PF 26-OCT-2000; 2000WO-US29451.  
 XX  
 PR 27-OCT-1999; 99US-0161775.  
 XX

XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 PI Demolf W, Kallender H, Lonsdale JT;  
 XX WPI: 2001-316332/33.  
 DR N-PSDB: AAD06214.  
 XX  
 PT High throughput method for screening for biological agents against  
 PT fatty acid biosynthesis comprises contacting a bacterial enzymatic  
 PT pathway with enzymes e.g. malonyl-CoA:ACP transacylase -  
 XX  
 PS Claim 1: Page 15; 94pp; English.  
 XX  
 CC The present invention relates to a high throughput method for screening  
 CC biological agents affecting fatty acid biosynthesis, comprises  
 CC contacting a bacterial enzymatic pathway with enzymes. The method is  
 CC used for screening biological agents affecting fatty acid biosynthesis.  
 CC Agonists and antagonists of fab (fatty acid biosynthesis) are used to  
 CC inhibit, prevent or treat diseases such as infections of the upper  
 CC respiratory tract (e.g. otitis media, bacterial tracheitis, acute  
 CC epiglottitis, thyroiditis), lower respiratory (e.g. empyema, lung  
 CC abscess), cardiac (e.g. infective endocarditis), gastrointestinal (e.g.  
 CC secretory diarrhoea, splenic abscess, retroperitoneal abscess), central  
 CC nervous system (e.g. cerebral abscess), eye (e.g. blepharitis,  
 CC conjunctivitis, keratitis, endophthalmitis, preseptal and orbital  
 CC cellulitis, dacryocystitis), kidney and urinary tract (e.g.  
 CC epididymitis, intrarenal and perinephric abscess, toxic shock syndrome),  
 CC skin (e.g. impetigo, folliculitis, cutaneous abscess, cellulitis, wound  
 CC infection, bacterial myositis) and bone and joint (e.g. septic  
 CC arthritis, osteomyelitis).  
 CC The present sequence is Escherichia coli MADPH-dependent  
 CC enoyl-ACP (acyl carrier protein) reductase (FabI). In fatty acid  
 CC biosynthetic pathway, dehydration by FabZ leads to trans-2-enoyl-ACP  
 CC which is in turn converted to acyl-ACP by FabI.  
 XX  
 SQ Sequence 262 AA:  
 Query Match 62.8%; Score 49; DB 22; Length 262;  
 Best Local Similarity 60.0%; Pred. No. 2.2;  
 Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 Oy 1 MRYRASALGSDGVRV 15  
 :|||:|:|:|:|  
 Db 170 VRYMANMGPGEVVR 184

RESULT 4  
 AAU38231  
 ID AAU38231 standard; Protein: 269 AA.  
 AC AAU38231;  
 XX  
 DT 14-FEB-2002 (first entry)  
 XX  
 DE Salmomella typhi cellular proliferation protein #122.  
 XX  
 KW Antisense: prokaryotic cellular proliferation protein;  
 KW antibiotic: antibacterial; drug design.  
 XX  
 OS Salmomella typhi.  
 XX  
 PM MO200170955-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 21-MAR-2001; 2001WO-US09180.  
 XX  
 PR 21-MAR-2000; 2000US-191078P.  
 PR 23-MAY-2000; 2000US-206848P.  
 PR 26-MAY-2000; 2000US-207227P.  
 PR 23-OCT-2000; 2000US-242578P.

PR 27-NOV-2000; 2000US-253625P.  
 PR 22-DEC-2000; 2000US-257931P.  
 PR 16-FEB-2001; 2001US-269308P.  
 XX  
 PA (ELITR) ELITRA PHARM INC.  
 XX  
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawlick JD, Carr CJ;  
 PI Yamamoto RT, Xu HH;  
 XX  
 DR WPI: 2001-611495/70.  
 XX N-PSDB: AAS56090.  
 XX  
 PT New polynucleotides for the identification and development of  
 PT antibiotics, comprise sequences of antisense nucleic acids -  
 XX  
 PS Example 3; Seq ID No 13824; 511pp; English.  
 XX  
 CC The invention relates to antisense inhibitors of genes essential to  
 CC prokaryotic cellular proliferation, their use in identifying the  
 CC genes, their use in the discovery of novel antibiotics, the essential  
 CC genes themselves and the encoded proteins. The prokaryotes used are  
 CC Escherichia coli, Staphylococcus aureus, Salmomella typhi, Klebsiella  
 CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The  
 CC invention is also useful for the identification of potential new targets  
 CC for antibiotic development. The antisense nucleic acids can also be used  
 CC to identify proteins used in proliferation, to express these proteins,  
 CC and to obtain antibodies capable of binding to the expressed proteins.  
 CC The proteins can be used to screen compounds in rational drug discovery  
 CC programmes. The antisense nucleic acid sequence is also useful to screen  
 CC for homologous nucleic acids which are required for cell proliferation in  
 CC a wide variety of organisms. The present sequence represents an  
 CC essential prokaryotic cellular proliferation protein.  
 CC Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 269 AA:  
 Query Match 62.8%; Score 49; DB 22; Length 269;  
 Best Local Similarity 60.0%; Pred. No. 2.3;  
 Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 Oy 1 MRYRASALGSDGVRV 15  
 :|||:|:|:|:|  
 Db 177 VRYMANMGPGEVVR 191

RESULT 5  
 AAY25520  
 ID AAY25520 standard; Protein: 429 AA.  
 AC AAY25520;  
 XX  
 DT 30-SEP-1999 (first entry)  
 XX  
 DE E. coli FabI protein fragment.  
 XX  
 KW FabI: enoyl ACP reductase; acyl carrier protein; antimicrobial; therapy;  
 KW fatty acid biosynthesis; detection; antibacterial; antifungal; treatment;  
 KW antiprotozoal; antiparasitic; antiviral; soap; infection; disinfectant;  
 KW detergent; mouthwash; toothpaste; contraceptive; inhibitor; triclosan;  
 KW resistance; NSAM; non-specific antimicrobial.  
 XX  
 OS Escherichia coli.  
 XX  
 FH Key  
 FH 1..429 Location/Qualifiers  
 FT Protein /label= FabI  
 FT /note= "No start or stop codon given in specification"  
 FT Misc-difference 74 /note= "in-frame stop codon encoded by TGA"  
 FT Misc-difference 111



PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001MO-US08631.  
XX  
PR 31-MAR-2000; 2000US-0540217.  
PR 23-AUG-2000; 2000US-0649167.  
PA  
XX (HYSE-) HYSEQ INC.  
PI Drmanac RT, Liu C, Tang YT.  
XX WPI; 2001-639362/73.  
DR N-PSDB; AAS92751.  
XX  
XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity -  
XX  
PS Claim 20; SEQ ID NO 58923; 103pp; English.  
XX  
XX The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG0010-ABG30377 represent novel human  
CC diagnostic amino acid sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
CC  
SQ Sequence 693 AA:  
Query Match 62.8%; Score 49; DB 22; Length 693;  
Best Local Similarity 60.0%; Pred. No. 6.2;  
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MRYRASALGSDGVY 15  
:|||:|:|:|:|  
Db 601 VRIMAMGPEGVY 615  
RESULT 8  
AAB90827  
ID AAB90827 standard; Protein: 267 AA.  
XX  
AC AAB90827;  
XX  
DT 15-JUN-2001 (first entry)  
XX  
DE Human shear stress-response protein SEQ ID NO: 171.  
XX  
KW Human; shear stress-response protein; vascular disease;  
KW arteriosclerosis.  
XX  
OS Homo sapiens.  
XX MO200125427-A1.  
XX  
PN 12-APR-2001.  
XX

PF 02-OCT-2000; 2000MO-JP06840.  
XX  
XX 01-OCT-1999; 99JP-0280976.  
XX  
XX (KYOM) KYOMA HAKKO KOGYO KK.  
PA (NOJI/) NOJIMA H.  
XX  
PI Nojima H, Yoshisue H, Obayashi M, Ota T, Kawabata A, Sakurada K;  
PI Kuga T, Sekine S, Nakamura Y, Sugano S;  
XX WPI; 2001-266308/72.  
DR N-PSDB; AAH02967.  
XX  
XX  
PT DNA sequences, proteins encoded by them and antibodies against them  
PT useful in diagnosis and treatment of vascular disease caused by  
PT arteriosclerosis -  
XX  
PS Claim 35; Page 664-665; 678pp; Japanese.  
XX  
XX The present invention provides the protein and coding sequences of a  
CC number of human shear stress response proteins. These are useful in the  
CC diagnosis, treatment and screening of vascular diseases caused by  
CC arteriosclerosis, including heart failure, post-PTCA restenosis and  
CC hypertension.  
XX  
SQ Sequence 267 AA:  
Query Match 61.5%; Score 48; DB 22; Length 267;  
Best Local Similarity 100.0%; Pred. No. 3.3;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 ALGSDGVY 16  
:|||||  
Db 26 ALGSDGVY 35  
RESULT 9  
AAM41777  
ID AAM41777 standard; Protein: 537 AA.  
XX  
AC AAM41777;  
XX  
DT 22-OCT-2001 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 6708.  
XX  
XX Human; neutrophil; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; hemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia.  
XX  
OS Homo sapiens.  
XX  
XX MO20015312-A1.  
XX  
PN 26-JUL-2001.  
XX  
PD 26-DEC-2000; 2000MO-US34263.  
XX  
PE 21-JAN-2000; 2000US-0488725.  
PR 25-APR-2000; 2000US-0552317.  
PR 09-JUL-2000; 2000US-0598042.  
PR 19-JUL-2000; 2000US-0620312.  
PR 03-AUG-2000; 2000US-0653450.  
PR 14-SEP-2000; 2000US-0662191.  
PR 19-OCT-2000; 2000US-0693036.  
PR 29-NOV-2000; 2000US-0727344.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;





PR 20-JUL-1999; 99US-0144352.  
 PR 20-JUL-1999; 99US-0144632.  
 PR 20-JUL-1999; 99US-0144884.  
 PR 21-JUL-1999; 99US-0144814.  
 PR 21-JUL-1999; 99US-0145086.  
 PR 21-JUL-1999; 99US-0145088.  
 PR 22-JUL-1999; 99US-0145085.  
 PR 22-JUL-1999; 99US-0145087.  
 PR 22-JUL-1999; 99US-0145089.  
 PR 22-JUL-1999; 99US-0145192.  
 PR 23-JUL-1999; 99US-0145145.  
 PR 23-JUL-1999; 99US-0145218.  
 PR 23-JUL-1999; 99US-0145224.  
 PR 26-JUL-1999; 99US-0145276.  
 PR 27-JUL-1999; 99US-0145813.  
 PR 27-JUL-1999; 99US-0145818.  
 PR 27-JUL-1999; 99US-0145919.  
 PR 28-JUL-1999; 99US-0145951.  
 PR 02-AUG-1999; 99US-0146386.  
 PR 02-AUG-1999; 99US-0146388.  
 PR 02-AUG-1999; 99US-0146389.  
 PR 03-AUG-1999; 99US-0147038.  
 PR 04-AUG-1999; 99US-0147204.  
 PR 04-AUG-1999; 99US-0147302.  
 PR 05-AUG-1999; 99US-0147192.  
 PR 05-AUG-1999; 99US-0147260.  
 PR 06-AUG-1999; 99US-0147303.  
 PR 06-AUG-1999; 99US-0147416.  
 PR 09-AUG-1999; 99US-0147493.  
 PR 09-AUG-1999; 99US-0147935.  
 PR 10-AUG-1999; 99US-0148171.  
 PR 11-AUG-1999; 99US-0148319.  
 PR 12-AUG-1999; 99US-0148341.  
 PR 13-AUG-1999; 99US-0148365.  
 PR 13-AUG-1999; 99US-0148684.  
 PR 16-AUG-1999; 99US-0149368.  
 PR 17-AUG-1999; 99US-0149175.  
 PR 18-AUG-1999; 99US-0149426.  
 PR 20-AUG-1999; 99US-0149722.  
 PR 20-AUG-1999; 99US-0149723.  
 PR 20-AUG-1999; 99US-0149929.  
 PR 23-AUG-1999; 99US-0149902.  
 PR 23-AUG-1999; 99US-0149930.  
 PR 25-AUG-1999; 99US-0150566.  
 PR 26-AUG-1999; 99US-0150884.  
 PR 27-AUG-1999; 99US-0151065.  
 PR 27-AUG-1999; 99US-0151066.  
 PR 27-AUG-1999; 99US-0151080.  
 PR 30-AUG-1999; 99US-0151303.  
 PR 31-AUG-1999; 99US-0151438.  
 PR 01-SEP-1999; 99US-0151930.  
 PR 07-SEP-1999; 99US-0152363.  
 PR 10-SEP-1999; 99US-0153070.  
 PR 13-SEP-1999; 99US-0153758.  
 PR 15-SEP-1999; 99US-0154039.  
 PR 16-SEP-1999; 99US-0154039.  
 PR 20-SEP-1999; 99US-0154779.  
 PR 22-SEP-1999; 99US-0155139.  
 PR 23-SEP-1999; 99US-0155486.  
 PR 24-SEP-1999; 99US-0155659.  
 PR 28-SEP-1999; 99US-0156458.  
 PR 29-SEP-1999; 99US-0156596.  
 PR 04-OCT-1999; 99US-0157117.  
 PR 05-OCT-1999; 99US-0157753.  
 PR 06-OCT-1999; 99US-0157865.  
 PR 07-OCT-1999; 99US-0158029.  
 PR 08-OCT-1999; 99US-0158232.  
 PR 12-OCT-1999; 99US-0158369.  
 PR 13-OCT-1999; 99US-0159293.  
 PR 13-OCT-1999; 99US-0159294.  
 PR 13-OCT-1999; 99US-0159295.  
 PR 14-OCT-1999; 99US-0159329.  
 PR 14-OCT-1999; 99US-0159330.

PR 14-OCT-1999; 99US-0159331.  
 PR 14-OCT-1999; 99US-0159637.  
 PR 14-OCT-1999; 99US-0159638.  
 PR 18-OCT-1999; 99US-0159584.  
 PR 21-OCT-1999; 99US-0160741.  
 PR 21-OCT-1999; 99US-0160767.  
 PR 21-OCT-1999; 99US-0160770.  
 PR 21-OCT-1999; 99US-0160814.  
 PR 21-OCT-1999; 99US-0160815.  
 PR 22-OCT-1999; 99US-0160980.  
 PR 22-OCT-1999; 99US-0160981.  
 PR 22-OCT-1999; 99US-0160989.  
 PR 25-OCT-1999; 99US-0161404.  
 PR 25-OCT-1999; 99US-0161405.  
 PR 25-OCT-1999; 99US-0161406.  
 PR 26-OCT-1999; 99US-0161359.  
 PR 26-OCT-1999; 99US-0161360.  
 PR 26-OCT-1999; 99US-0161361.  
 PR 28-OCT-1999; 99US-0161920.  
 PR 28-OCT-1999; 99US-0161992.  
 PR 28-OCT-1999; 99US-0161993.  
 PR 29-OCT-1999; 99US-0162142.

Query Match 57.7%; Score 45; DB 21; Length 357;  
 Best Local Similarity 69.2%; Pred. No. 15;  
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 RASALGSDGVRYT 16  
 DB 43 RASALGNTGLKVT 55

# RESULT 13

ID AU036258 standard; Protein; 265 AA.

AC AU036258;

DT 14-FEB-2002 (first entry)

DE Pseudomonas aeruginosa cellular proliferation protein #248.

KW Antisense; prokaryotic cellular proliferation protein;

KW antibiotic; antibacterial; drug design.

XX Pseudomonas aeruginosa.

OS WO200170955-A2.

PN 27-SEP-2001.

PD 21-MAR-2001; 2001WO-US09180.

PF 21-MAR-2000; 2000US-191078P.

PR 23-MAY-2000; 2000US-206848P.

PR 26-MAY-2000; 2000US-207727P.

PR 23-OCT-2000; 2000US-242578P.

PR 27-NOV-2000; 2000US-253625P.

PR 22-DEC-2000; 2000US-257931P.

PR 16-FEB-2001; 2001US-269308P.

PA (ELIT- ) ELITRA PHARM INC.

PI Hasselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

PI Yamamoto RT, Xu HH;

DR WPI; 2001-611495/70.

DR N-PSDB; AAS54117.

PT New polynucleotides for the identification and development of

PT antibiotics, comprise sequences of antisense nucleic acids -

PS Example 3: Seq ID NO 11851: 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to

CC prokaryotic cellular proliferation, their use in identifying the

CC genes, their use in the discovery of novel antibiotics, the essential

CC genes themselves and the encoded proteins. The prokaryotes used are

CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*

CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The

CC invention is also useful for the identification of potential new targets

CC for antibiotic development. The antisense nucleic acids can also be used

CC and to obtain antibodies capable of binding to the expressed proteins.

CC The proteins can be used to screen compounds in rational drug discovery

CC for homologous nucleic acids which are required for cell proliferation in

CC a wide variety of organisms. The present sequence represents an

CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic

CC format directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences.

XX

SO Sequence 265 AA:

Query Match 56.4%; Score 44; DB 22; Length 265;

Best Local Similarity 53.3%; Pred. No. 16;

Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 MRYRASALGSDGVRV 15

Db 173 VRYIAGSLAGEGTRV 187

||| | :||:| |

RESULT 14

AAW9839

ID AAW9839 standard; Protein: 268 AA.

XX

AC- AAW9839;

XX

DT 08-JUN-1999 (first entry)

XX

DE L. pneumophila FabI enoyl reductase homologue protein sequence.

XX

KW *Legionella pneumophila*; FabI; enoyl reductase; antimicrobial;

KM *gemfibrozil*; growth inhibition; bacterium; infection.

XX

OS *Legionella pneumophila*.

XX

PN WO9731530-A1.

XX

PD 04-SEP-1997.

XX

PF 28-FEB-1997; 97WO-US03158.

XX

PR 29-FEB-1996; 96US-0608712.

XX

PA (UYCO ) UNIV COLUMBIA NEW YORK.

XX

PI Della-Latta P, Kabbash C, Shuman HA, Silverstein SC;

XX

DR WPI: 1997-448377/41.

XX

DR N-PSDB: AAX19775.

XX

PT Inhibiting growth of bacteria - by contacting the bacteria with

XX

PS *gemfibrozil* or related compound

XX

XX Example 2: Fig 21B: 109pp; English.

XX

CC A method has been developed for: (1) inhibiting growth of a bacterium;

CC (11) alleviating the symptoms of a bacterial infection in a subject;

CC (111) inhibiting activity of enoyl reductase enzyme in a cell; or (1v)

CC altering a pathway of fatty acid synthesis in a bacterium, comprises

CC contacting the bacterium, subject or cell with a novel compound (I) or

CC its salt or ester. The above processes are especially applicable to

CC bacteria/bacterial cells selected from *Legionella pneumophila*,

CC *Mycobacterium tuberculosis*, *Bacillus subtilis*, *Bacillus megaterium*,

CC *Pseudomonas oleovorans*, *Alcaligenes eutrophus*, *Rhodococcus sp.*,

CC *Citrobacter freundii*, Group A *Streptococcus sp.*, *Coxsack* *Staphylococcus*

CC *aureus* or *Neisseria sp.* The bacterial infection is e.g. leprosy, brucella

CC or *salmonella*. The present sequence represents a FabI enoyl reductase

CC homologue from *L. pneumophila*, which is used in an example from the

CC present invention.

XX

SO Sequence 268 AA:

Query Match 56.4%; Score 44; DB 18; Length 268;

Best Local Similarity 53.3%; Pred. No. 16;

Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 MRYRASALGSDGVRV 15

Db 177 VRYIAGSLAGEGTRV 191

||| | :||:| |

RESULT 15

ABB93255

ID ABB93255 standard; Protein: 415 AA.

XX

AC ABB93255;

XX

DT 31-MAY-2002 (first entry)

XX

DE Herbicidally active polypeptide SEQ ID NO 2466.

XX

XX Herbicidal; plant; agriculture; herbicide.

XX

OS *Arabidopsis thaliana*.

XX

PN WO200210210-A2.

XX

PD 07-FEB-2002.

XX

PF 28-AUG-2001; 2001WO-EP09892.

XX

PR 28-AUG-2001; 2001WO-EP09892.

XX

PA (FARB ) BAYER AG.

XX

PI Tietjen K, Weidner M;

XX

DR WPI: 2002-269010/31.

XX

PT Identifying plant target proteins for herbicidally active compounds,

XX

PT comprising aligning and comparing nucleic acid or amino acid sequences

XX

PT from plant with nucleic acid or amino acid sequences from non-plant

XX

PS organisms -

XX

PS Claim 5; SEQ ID NO 2466; 261pp + Sequence Listing; English.

XX

XX

CC The invention relates to identifying target proteins

CC (ABB90790-ABB94016) for herbicidally active compounds, comprising

CC aligning and comparing nucleic acid or amino acid sequences from plant

CC with nucleic acid or amino acid sequences from non-plant organisms using

CC suitable search parameters, where plant sequences having an E-value

CC greater by a factor of 3 than the E-value of most similar non-plant

CC sequences are selected. The polypeptides or nucleic acids encoding them

CC are useful for identifying modulators. The identified modulators are

CC useful as herbicides.

XX

SO Sequence 415 AA:

Query Match 52.6%; Score 41; DB 23; Length 415;

Best Local Similarity 53.3%; Pred. No. 82;

Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 2 RYRASALGSDGVRV 16

Thu Jan 16 15:49:08 2003

us-09-893-371-2.rag

Page 10

||:||||:|  
Db 392 RYKAGALGAERKRAT 406

Search completed: January 16, 2003, 10:12:11  
Job time : 38 secs

---

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 16, 2003, 10:10:53 ; Search time 29 seconds

(without alignments)  
113.681 Million cell updates/sec

Title: US-09-893-371-2

Perfect score: 78

Sequence: 1 MRYRASALGSDGVAVT 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL\_21:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mmc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_virus:\*

16: sp\_bacteriophage:\*

17: sp\_archaeophages:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	1044	11	Q9ERB6 mus musculus
2	50	64.1	260	16	Q9CP73 pasteurella
3	49	62.8	262	16	Q87C7 salmonella
4	48	61.5	264	2	Q1891 proteus mir
5	45	57.7	264	16	Q8Y072 raietonia s
6	44	56.4	268	2	Q8WQ34 leishmania
7	44	55.1	268	2	Q9RE03 legionella
8	42	53.8	291	10	Q9L5F6 burkholderi
9	42	53.8	291	10	Q9L5F6 burkholderi
10	41	52.6	151	2	Q9L5F6 burkholderi
11	41	52.6	151	16	Q9L5F6 burkholderi
12	41	52.6	252	16	Q9L5F6 burkholderi
13	41	52.6	258	16	Q9L5F6 burkholderi
14	41	52.6	356	10	Q9L5F6 burkholderi
15	41	52.6	415	10	Q9L5F6 burkholderi
16	41	52.6	419	10	Q9L5F6 burkholderi

17	41	52.6	572	16	Q9S1S8 streptomyc
18	40	51.3	375	16	Q9F2K4 streptomyc
19	40	51.3	412	4	Q96PW2 homo sapien
20	40	51.3	437	16	Q9KY22 streptomyc
21	40	51.3	467	5	Q9GTX9 armigeres s
22	39	50.0	242	2	Q9L8E7 vibrio harv
23	39	50.0	261	16	Q9K151 neisseria m
24	39	50.0	261	16	Q9JSS8 neisseria m
25	39	50.0	262	16	Q9JSS8 neisseria m
26	39	50.0	262	16	Q9JSS8 neisseria m
27	39	50.0	274	16	Q9JSS8 neisseria m
28	39	50.0	467	10	Q9JSS8 neisseria m
29	39	50.0	551	2	Q9JSS8 neisseria m
30	39	50.0	793	2	Q9JSS8 neisseria m
31	39	50.0	793	2	Q9JSS8 neisseria m
32	39	50.0	844	10	Q9JSS8 neisseria m
33	39	50.0	875	10	Q9JSS8 neisseria m
34	39	50.0	924	16	Q9JSS8 neisseria m
35	39	50.0	1296	16	Q9JSS8 neisseria m
36	39	50.0	1470	5	Q9JSS8 neisseria m
37	39	50.0	2395	2	Q9JSS8 neisseria m
38	38	49.4	513	16	Q9JSS8 neisseria m
39	38	48.7	110	16	Q9JSS8 neisseria m
40	38	48.7	146	10	Q9JSS8 neisseria m
41	38	48.7	192	5	Q9JSS8 neisseria m
42	38	48.7	254	16	Q9JSS8 neisseria m
43	38	48.7	272	16	Q9JSS8 neisseria m
44	38	48.7	298	10	Q9JSS8 neisseria m
45	38	48.7	312	16	Q9JSS8 neisseria m

## ALIGNMENTS

## RESULT 1

ID	Q9ERB6	PRELIMINARY:	PRT:	1044 AA.
AC	Q9ERB6	Q9ERB6		
DT	01-MAR-2001	(TREMURel. 16, Created)		
DT	01-MAR-2001	(TREMURel. 16, Last sequence update)		
DT	01-JUN-2002	(TREMURel. 21, Last annotation update)		
DE	Nuclear myosin I beta.			
GN	MYOIC.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Pestic-Dragovich L., Stojiljkovic L., Philimonenko A.A., Nowak G.,			
RA	Ke Y., Settlage R.E., Shabanowitz J., Hunt D.F., Hozak P.,			
RA	de lanerolle P.,			
RT	"A Myosin I Isoform in the Nucleus."			
RL	Science 0:0-0(2000).			
DR	EMBL: AY007255; AAG02570.1; -			
DR	HSSP: P08799; 1MND.			
DR	MCD: MGI:106612; MYOIC.			
DR	InterPro: IPR000048; IQ_region.			
DR	InterPro: IPR001609; myosin_head.			
DR	Pfam: PF00612; IQ_3.			
DR	Pfam: PF00663; myosin_head; 1.			
DR	PRINTS: PR00193; MYOSINHEAVY.			
DR	ProDom: PD000355; myosin_head; 1.			
DR	SMART: SM00015; IQ_2.			
DR	SMART: SM00242; MISC: 1.			
SQ	SEQUENCE 1044 AA: 119876 MW: CDAB0F699D041C9 CRC64;			

Query Match 100.0%; Score 78; DB 11; Length 1044;  
Best Local Similarity 100.0%; Pred. No. 0.00014;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYRASALGSDGVAVT 16  
|||||

Db 1 MRYRASALGSDGVRV 16

RESULT 2

ID 09CP73 PRELIMINARY; PRT; 260 AA.

AC 09CP73:

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Fabi.

GN PABI OR PM0182.

OS Pasteurella multocida.

OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;

OC Pasteurella.

OX NCBI\_TaxID=747;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PM70;

RX MEDLINE=21145866; PubMed=11248100;

RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;

RT "Complete genome sequence of Pasteurella multocida PM70.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.

CC EMBL; AF006052; AK02266.1; -.

DR HSP; P29132; 10SG.

DR InterPro: IPR002198; ADH\_short.

DR Pfam: PF00106; adh\_short; 1.

KW Oxidoreductase; Complete proteome.

SO SEQUENCE 260 AA; 27850 MW; 922E5EBE8B0C8963 CRC64;

Query Match 64.1%; Score 50; DB 16; Length 260;

Best Local Similarity 64.3%; Pred. No. 1.7;

Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 RYRASALGSDGVRV 15

Db 171 RFMAALGKDGIRV 184

RESULT 3

ID 0827C7 PRELIMINARY; PRT; 262 AA.

AC 0827C7:

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Enoyl-[acyl-carrier-protein] reductase (NADH).

GN sry1352.

OS Salmonella typhi.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Salmonella.

OX NCBI\_TaxID=601;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Ct18;

RX MEDLINE=21534947; PubMed=11677608;

RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,

RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,

RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,

RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,

RA Feltwell T., Hamlin P., Hague A., Hen T.T., Holroyd S., Jagels K.,

RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,

RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,

RA Whitehead S., Barrett B.G.;

RT "Complete genome sequence of a multiple drug resistant Salmonella

RT enterica serovar Typhi Ct18.";

RL Nature 413:848-852(2001).

DR EMBL; AL672770; CAP01621.1; -.

DR InterPro: IPR002198; ADH\_short.

DR Pfam: PF00106; adh\_short; 1.

KW Complete proteome.

SO SEQUENCE 262 AA; 27775 MW; 1844E8792E709A93 CRC64;

Query Match 62.8%; Score 49; DB 16; Length 262;

Best Local Similarity 60.0%; Pred. No. 2.6;

Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRYRASALGSDGVRV 15

Db 170 VRYMANMGPEGIRV 184

RESULT 4

ID 051891 PRELIMINARY; PRT; 99 AA.

AC 051891:

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Similar to E.coli EnvM (Fragment).

OS Proteus mirabilis.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Proteus.

OX NCBI\_TaxID=584;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=AF 2924;

RX MEDLINE=93170270; PubMed=8436105;

RA Mignogna G., Allocali N., Aceto A., Piccolomini R., Di Ilio C.,

RA Baria D., Martini F.;

RT "The amino acid sequence of glutathione transferase from Proteus

RT mirabilis, a prototype of a new class of enzymes.";

RL Eur. J. Biochem. 211:421-425(1993).

RP [2]

RP SEQUENCE FROM N.A.

RC STRAIN=AF 2924;

RX MEDLINE=96358500; PubMed=8761466;

RA Perito B., Allocali N., Aceto A., Casalone E., Di Ilio C., Masulli M.,

RA Dragani B., Polinelli M.;

RT "Molecular cloning and overexpression of a glutathione transferase

RT gene from Proteus mirabilis.";

RL Biochem. J. 318:157-162(1996).

DR EMBL; U38482; AAC44361.1; -.

DR HSP; P29132; 1DFT.

DR InterPro: IPR002198; ADH\_short.

DR Pfam: PF00106; adh\_short; 1.

FT NON\_TER 1

SO SEQUENCE 99 AA; 10395 MW; 2E442ABB04FA031 CRC64;

Query Match 61.5%; Score 48; DB 2; Length 99;

Best Local Similarity 53.3%; Pred. No. 1.3;

Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRYRASALGSDGVRV 15

Db 7 VRYMANMGPEGIRV 21

RESULT 5

ID 08Y072 PRELIMINARY; PRT; 264 AA.

AC 08Y072:

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Probable enoyl-[acyl-carrier-protein] reductase (EC 1.3.1.9).

GN PABI OR RSC1172 OR RS04528.

OS Ralstonia solanacearum (Pseudomonas solanacearum).

OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;

OC Ralstonia.

OX NCBI\_TaxID=305;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=GM11000;

RX MEDLINE=21681879; PubMed=11823852;  
 RA Salanoubat M., Genin S., Attienave F., Guzy J., Mangenot S.,  
 RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,  
 RA Chandelier M., Choisme N., Claudel-Renard C., Cunac S., Demange N.,  
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,  
 RA Siguer P., Thebaud P., Whalen M., Winkler P., Levy M.,  
 RA Weissenbach J., Boucher C.A.;  
 RT "Genome sequence of the plant pathogen *Ralstonia solanacearum*";  
 RL Nature 415:497-502(2002).  
 DR EMBL; AL646063; CAD14874.1; -  
 DR InterPro; IPR002198; ADH\_short.  
 DR Pfam; PF00106; adh\_short; 1.  
 KW Oxidoreductase; Complete proteome  
 SQ SEQUENCE 264 AA; 28006 MW; 1CE90B4C10AE3A52 CRC64;  
 QY Query Match 57.7%; Score 45; DB 16; Length 264;  
 Best Local Similarity 64.3%; Pred. No. 13;  
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 Db 1 MRYRASALGSDGVR 14  
 :| | | | | | | |  
 170 VRYLASALGPKGR 183  
 RESULT 6  
 Q8WQ34 PRELIMINARY; PRT; 444 AA.  
 AC Q8WQ34;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DE Hypothetical predicted transmembrane protein P265.17, unknown  
 DE function.  
 GN P265.17.  
 OS Leishmania major.  
 OC Eukaryota; Eukaryota; Kinetoplastida; Trypanosomatidae; Leishmania.  
 OX NCBI\_TaxID=5664;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FRIEDLIN;  
 RA Robben J., Grymoprez B., Weltjens I., Aert R., Volckaert G.,  
 RA Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FRIEDLIN;  
 RX MEDLINE=98146435; PubMed=9477341;  
 RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,  
 RA Smith D.F.;  
 RT "A physical map of the *Leishmania major* Friedlin genome";  
 RL Genome Res. 8:135-145(1998).  
 DR EMBL; AL359716; CAD19425.1; -  
 KW Transmembrane.  
 SQ SEQUENCE 444 AA; 49507 MW; 5E0CBA3C2868398A CRC64;  
 QY Query Match 57.7%; Score 45; DB 5; Length 444;  
 Best Local Similarity 56.2%; Pred. No. 22;  
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 Db 1 MRYRASALGSDGVR 16  
 :| | | | | | | |  
 22 MYSASLSSSGIEVT 37  
 RESULT 7  
 Q9RE03 PRELIMINARY; PRT; 268 AA.  
 AC Q9RE03;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DE Enoyl reductase.  
 GN FABI.

OS Legionella pneumophila.  
 OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;  
 OC Legionellaceae; Legionella.  
 OX NCBI\_TaxID=446;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PHILADELPHIA 1 SGI;  
 RA Kabbash C.A., Albala A., Latta P.D., Feinmark S., Weiss I., Walthe E.,  
 RA Silverstein S.C., Shuman H.A.;  
 RT "Antibiotic activity of gemfibrozil for *L.pneumophila* and  
 RT *M.tuberculosis*";  
 RL Submitted (MUG-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES  
 CC (SDR) FAMILY.  
 DR EMBL; Y14405; CAB65183.1; -  
 DR HSSP; P29132; 10SG.  
 DR InterPro; IPR002198; ADH\_short.  
 DR Pfam; PF00106; adh\_short; 1.  
 KW Oxidoreductase.  
 SQ SEQUENCE 268 AA; 28466 MW; DF6B4E16AE589E2D CRC64;  
 QY Query Match 56.4%; Score 44; DB 2; Length 268;  
 Best Local Similarity 53.3%; Pred. No. 19;  
 Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
 Db 1 MRYRASALGSDGVR 15  
 :| | | | | | | |  
 177 VRYLASLGSGLRI 191  
 RESULT 8  
 Q9FLK5 PRELIMINARY; PRT; 826 AA.  
 ID Q9FLK5;  
 AC Q9FLK5;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DE Hypothetical protein, last annotation update)  
 DE Chitinase.  
 GN BCC1.  
 OS Burkholderia cepacia (Pseudomonas cepacia).  
 OC Bacteria; Proteobacteria; beta subdivision; Burkholderia group;  
 OC Burkholderia.  
 OX NCBI\_TaxID=292;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Matsuda Y., Kakutani K., Nonomura T., Ikeda S., Tamai T., Kuyabara Y.,  
 RA Tanaka H., Toyoda H.;  
 RT "DNA sequence of chitinase gene cloned from *Burkholderia cepacia*";  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB053088; BAB20043.1; -  
 DR HSSP; O54468; 10BA.  
 DR InterPro; IPR004866; CarDB\_Hex.  
 DR InterPro; IPR001540; GH\_20.  
 DR Pfam; PF03173; CHB\_Hex; 1.  
 DR Pfam; PF00728; Glyco\_hydro\_20; 1.  
 DR PRINTS; PR00736; GLHYDRLSE20.  
 SQ SEQUENCE 826 AA; 90168 MW; E9CC7A6544DC31EC CRC64;  
 QY Query Match 55.1%; Score 43; DB 2; Length 826;  
 Best Local Similarity 60.0%; Pred. No. 97;  
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 Db 1 MRYRASALGSDGVR 15  
 :| | | | | | | |  
 252 LRDRATTLGLDGARV 266  
 RESULT 9  
 Q9LPK0 PRELIMINARY; PRT; 291 AA.  
 ID Q9LPK0;  
 AC Q9LPK0;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)



DB 167 RLHNAHFGPDGIRV 180

RESULT 13  
0930L5 PRELIMINARY: PRT: 258 AA.

AC 0930L5: 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE Puteative.  
GN RA0180 OR SMA0335.  
OS Rhizobium meliloti (Sinorhizobium meliloti).  
OC Plasmid psyma (megaplasmid 1).  
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
OC Rhizobiaceae; Sinorhizobium.  
OX NCBI\_TaxID=382;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1021;  
RX MEDLINE=21396509; PubMed=11481432;  
RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,  
RA Barclay-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,  
RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,  
RA Kahan S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,  
RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;  
RT "Nucleotide sequence and predicted functions of the entire  
RT Sinorhizobium meliloti psyma megaplasmid."  
RT Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).  
DR EMBL: AE007211; AAK64838.1;  
DR InterPro: IPR002198; ADH\_short.  
DR Pfam: PF00106; adh\_short; 1.  
DR PROSITE: PS00061; ADH\_SHORT; UNKNOWN\_1.  
KW Plasmid; Hypothetical protein; Complete proteome.  
SQ SEQUENCE 258 AA; 26146 MW; 446BAHCL4A2A8BB1 CRC64;

Query Match 52.6%; Score 41; DB 16; Length 258;  
Best Local Similarity 72.7%; Pred. No. 59;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 5 ASALGSDGVRV 15  
DB 177 ADALGPDGIRV 187

RESULT 14  
081792 PRELIMINARY: PRT: 356 AA.  
AC 081792: 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE Protein kinase - like protein (Fragment).  
GN F8D20.110.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Koeltter P., Hempel S., Entian K.-D., Hohelsel J., Jesse T.,  
RA Heijnen L., Vos P., Mewes H.W., Mayer K.F.X., Schueller C., Bevan M.;  
RN Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
RP SEQUENCE FROM N.A.  
RA EU Arabidopsis sequencing project;  
CC Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
EMBL: AL031135; CAA20030.1;  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_kinase.  
DR InterPro: IPR004040; STY\_pkinase.

DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF00069; pkinase; 1.  
DR PRINTS: PR00109; TYRKINASE.  
DR PRODOM: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00221; STYK; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_SF; 1.  
KW Kinase; Serine/threonine-protein kinase.  
FT NON\_PTER 1  
SQ SEQUENCE 356 AA; 40012 MW; FAD9736384FB8221 CRC64;

Query Match 52.6%; Score 41; DB 10; Length 356;  
Best Local Similarity 53.3%; Pred. No. 84;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 2 RYKAGALGAEKRRAT 16  
DB 333 RYKAGALGAEKRRAT 347

RESULT 15  
09M068 PRELIMINARY: PRT: 415 AA.  
AC 09M068: 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE Protein kinase-like protein.  
GN AY4635600.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.;  
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RP SEQUENCE FROM N.A.  
RA EU Arabidopsis sequencing project;  
CC Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
EMBL: AL161587; CAB80276.1;  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_kinase.  
DR InterPro: IPR004040; STY\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF00069; pkinase; 1.  
DR PRINTS: PR00109; TYRKINASE.  
DR PRODOM: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00221; STYK; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_SF; 1.  
KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 415 AA; 45879 MW; 2FAPD025A219F528 CRC64;

Query Match 52.6%; Score 41; DB 10; Length 415;  
Best Local Similarity 53.3%; Pred. No. 99;  
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 2 RYKAGALGAEKRRAT 16  
DB 392 RYKAGALGAEKRRAT 406

Search completed: January 16, 2003, 10:13:05  
Job time : 31 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 16, 2003, 10:08:27 ; Search time 11 Seconds

(without alignments)  
60.329 Million cell updates/sec

Title: US-09-893-371-2

Perfect score: 78

Sequence: 1 MRRASALGSDGVRT 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	62.8	261	1	FABI_ECOLI
2	49	62.8	261	1	FABI_SALTY
3	45	57.7	260	1	FABI_BUCAT
4	44	56.4	258	1	FABI_ANASP
5	44	56.4	265	1	FABI_PSEAE
6	44	56.4	1391	1	YID5_CAEEL
7	41	52.6	548	1	AMT4_PSEST
8	39	50.0	268	1	FAI2_RHIME
9	38	48.7	109	1	RLAI_MAIZE
10	38	48.7	155	1	CYSC_ARCFU
11	38	48.7	229	1	TPIS_SULTO
12	38	48.7	272	1	FAI1_RHIME
13	38	48.7	424	1	GSA_CAMEL
14	38	48.7	474	1	CYAE_BORPE
15	38	48.7	513	1	YME6_MYCTU
16	37	47.4	545	1	DCIP_AZOBH
17	37	47.4	353	1	H182_MYCTU
18	37	47.4	551	1	AMT4_PSESA
19	37	47.4	622	1	C2AC_BACTU
20	37	47.4	2212	1	RRPL_EBOZM
21	36	46.2	229	1	HIS4_PYRAE
22	36	46.2	237	1	YPV4_METTF
23	36	46.2	258	1	FABI_SYNY3
24	36	46.2	261	1	FABI_HAEIN
25	36	46.2	334	1	BCHI_RHOSH
26	36	46.2	350	1	BCHI_RHOCB
27	36	46.2	361	1	RPL_MYCLE
28	36	46.2	401	1	DXR_STRCO
29	36	46.2	427	1	TOLB_HAEIN
30	36	46.2	617	1	ESRI_ICTPU
31	36	46.2	710	1	DAS_PICAN
32	36	46.2	715	1	AT12_HSV1F
33	36	46.2	718	1	AT12_HSV1I

34	36	46.2	778	1	HTR6_HALNI
35	36	46.2	778	1	HTR6_HALSA
36	36	46.2	817	1	PPSA_PYRFU
37	36	46.2	819	1	PPSA_PYRAB
38	36	46.2	821	1	PPSA_PYRHO
39	36	46.2	1004	1	SLPO_BACBR
40	36	46.2	1188	1	PPSA_METJA
41	35	44.9	258	1	FABI_BACSU
42	35	44.9	285	1	GS39_BACSU
43	35	44.9	353	1	VGIM_KCMVK
44	35	44.9	360	1	MTDH_ARATH
45	35	44.9	368	1	RF2_STRCO

## ALIGNMENTS

RESULT 1	ID	FABI_ECOLI	STANDARD:	PRT:	261 AA.
AC	P29132;				
DT	01-DEC-1992 (Rel. 24, Created)				
DT	01-FEB-1996 (Rel. 33, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Enoyl-[acyl-carrier-protein] reductase [NADH] (EC 1.3.1.9) (NADH-dependent enoyl-ACP reductase).				
GN	FABI OR ENVW OR B1288 OR Z2512 OR ECS1861.				
OS	Escherichia coli, and				
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia				
OC	NCBI_TaxID=562, 83334;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 1-30.				
RX	MEDLINE=931233967; PubMed=1364817;				
RA	Bergler H., Hoegenauer G., Turnowsky F.;				
RT	"Sequences of the envm gene and of two mutated alleles in Escherichia coli.";				
RL	J. Gen. Microbiol. 138:2093-2100(1992).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=K12 / W3110;				
RX	MEDLINE=94355651; PubMed=8075395;				
RA	Kater M.W., Konigstein G.M., Nijkamp H.J.J., Stultje A.R.;				
RT	"The use of a hybrid genetic system to study the functional relationship between prokaryotic and plant multi-enzyme fatty acid synthase complexes.";				
RL	Plant Mol. Biol. 25:771-790(1994).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=K12 / MG1655;				
RX	MEDLINE=97426617; PubMed=9278503;				
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Mau B., Shao Y.;				
RT	"The complete genome sequence of Escherichia coli K-12.";				
RL	Science 277:1453-1474(1997).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=K12;				
RX	MEDLINE=97251357; PubMed=9097039;				
RA	Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itch T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y., Sivasubraman S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;				
RT	"A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";				
RL	DNA Res. 3:363-377(1996).				
RN	[5]				
RP	SEQUENCE FROM N.A.				

```

RL      Nature 398:383-384,(1999).
CC      CC      -1- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + NAD(+) = trans-
CC      CC      2,3-dehydroacyl-[acyl-carrier protein] + NADH.
CC      CC      -1- PATHWAY: SECOND REDUCTIVE STEP IN FATTY ACID BIOSYNTHESIS.
CC      CC      -1- SUBUNIT: HOMOTETRAMER.
CC      CC      -1- SUBCELLULAR LOCATION: Inner membrane-associated.
CC      CC      -1- MISCELLANEOUS: THE ANTIBIOTIC DIAZABORINE INTERFERES WITH THE
CC      CC      ACTIVITY BY BINDING TO THE PROTEIN.
CC      CC      -1- SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN
CC      CC      DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
CC      CC      -----
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CC      CC      -----
DR      DR      EMBL; M97219; AAA17755.1; -.
DR      DR      EMBL; X78733; CAA55381.1; -.
DR      DR      EMBL; AE000227; AAC74370.1; -.
DR      DR      EMBL; D90766; BAA14841.1; -.
DR      DR      EMBL; D90767; BAA14849.1; -.
DR      DR      EMBL; AE005378; AAG56524.1; -.
DR      DR      EMBL; AP002556; BAB35284.1; -.
DR      DR      PIR; A47681; A47681.
DR      DR      PDB; 1DEG; 28-JAN-98.
DR      DR      PDB; 1DFI; 28-JAN-98.
DR      DR      PDB; 1DFI; 28-JAN-98.
DR      DR      PDB; 1Q66; 21-SEP-99.
DR      DR      PDB; 1QSG; 21-JUL-99.
DR      DR      PDB; 1D8A; 28-OCT-99.
DR      DR      SWISS-2DPAGE; P29132; COLI.
DR      DR      Ecogene; EG11528; fabI.
DR      DR      InterPro; IPR002198; ADH_short.
DR      DR      Pfam; PF00106; adh_short.1.
KW      KW      Oxidoreductase; NAD; Fatty acid biosynthesis; Antibiotic resistance;
KW      KW      Inner membrane; 3D-structure; Complete proteome.
FT      FT      INIT_MET 0
FT      FT      NP_BIND 9 35 NAD (BY SIMILARITY)
FT      FT      MTTAGEN 92 92 G->S: DIAZABORINE RESISTANCE
FT      FT      MTTAGEN 240 240 S->F: PRODUCES TEMPERATURE-SENSITIVE
FT      FT      MTTAGEN PHENOTYPE.
SQ      SQ      SEQUENCE 261 AA; 27732 MW; 434B019F34855956 CRC64;
      Query Match 62.8%; Score 49; DB 1; Length 261;
      Best Local Similarity 60.0%; Pred. No. 0.29;
      Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0
Oy      1 MRYRASALGSDGVRV 15
      :| :|:|:| :|||
Db      169 VRYMANMGEPEGRV 183

RESULT 2
FABI_SALTY
ID FABI_SALTY STANDARD; PRT; 261 AA.
AC P16657;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Enoyl-[acyl-carrier-protein] reductase [NADH] (EC 1.3.1.9) (NADH-
DE dependent enoyl-ACP reductase).
DE FABI OR ENVM OR STM1700.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBL_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AG701;
RX MEDLINE=90078098; PubMed=2687243;

```

RA Turnowsky F., Fuchs K., Jeschek C., Hoegenauer G.;  
 RT "envm genes of *Salmonella typhimurium* and *Escherichia coli*.";   
 RN J. Bacteriol. 171:6555-6565(1989).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;  
 RA MEDLINE=21534948; PubMed=11677609;  
 RX McCalland M., Sanderson K.E., Spieeth J., Clifton S.W., Latrelle P.,  
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
 RA Waterston R., Wilson R.K.;  
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium  
 LT2.";  
 RL Nature 413:852-856(2001).  
 CC -1- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + NAD(+) = trans-  
 CC 2,3-dehydroacyl-[acyl-carrier protein] + NADH.  
 CC -1- PATHWAY: SECOND REDUCTIVE STEP IN FATTY ACID BIOSYNTHESIS.  
 CC -1- SUBCELLULAR LOCATION: Inner membrane-associated.  
 CC -1- MISCELLANEOUS: THE ANTIBIOTIC DIAZABORINE INTERFERES WITH THE  
 CC ACTIVITY BY BINDING TO THE PROTEIN.  
 CC -1- SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN  
 CC DEHYDROGENASES/REDUCTASES (SDR) FAMILY.  
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 CC -----  
 DR EMBL: M31806; AAA27059.1; -;  
 DR EMBL: AE008775; AA120618.1; -;  
 DR PIR: B43729; B43729.  
 DR HSSP: P29132; IDFI.  
 DR StyGene: SG10095; fabI.  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short. 1.  
 DR Oxidoreductase: NAD: Fatty acid biosynthesis; Antibiotic resistance;  
 KW Inner membrane; Complete proteome.  
 FT INIT\_MET 0 0 BY SIMILARITY.  
 FT NP\_BIND 9 35 NAD (BY SIMILARITY).  
 FT MUTAGEN 92 92 G->S; DIAZABORINE RESISTANCE.  
 SQ SEQUENCE 261 AA; 27629 MW; 187B91AEB341B773 CRC64;  
 Query Match 62.8%; Score 49; DB 1; Length 261;  
 Best Local Similarity 60.0%; Pred. No. 0.29;  
 Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 Oy 1 MRYRASALGSDGVRV 15  
 Db 169 VRYMANAMPEGVYR 183  
 RESULT 3  
 FABI\_BUCAI  
 ID FABI\_BUCAI STANDARD; PRT; 260 AA.  
 AC P57533;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Enoyl-[acyl-carrier-protein] reductase [NADH] (EC 1.3.1.9) (NADH-  
 DE dependent enoyl-ACP reductase).  
 GN FABI OR BU265  
 OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum  
 OS symbiotic bacterium).  
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.  
 OX NCBI\_TaxID=118099;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Tokyo 1998;  
 RX MEDLINE=20445173; PubMed=10993077;

RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;  
 RT "Genome sequence of the endocellular bacterial symbiont of aphids  
 RT Buchnera sp. APS.";  
 RN Nature 407:81-86(2000).  
 RL Nature 407:81-86(2000).  
 CC -1- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + NAD(+) = trans-  
 CC 2,3-dehydroacyl-[acyl-carrier protein] + NADH.  
 CC -1- PATHWAY: SECOND REDUCTIVE STEP IN FATTY ACID BIOSYNTHESIS.  
 CC -1- SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN  
 CC DEHYDROGENASES/REDUCTASES (SDR) FAMILY.  
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 CC -----  
 DR EMBL: AP001118; BAB12975.1; -;  
 DR HSSP: P29132; IDFI.  
 DR Oxidoreductase: NAD: Fatty acid biosynthesis; Complete proteome.  
 FT NP\_BIND 10 36 NAD (BY SIMILARITY).  
 SQ SEQUENCE 260 AA; 28779 MW; DCA04AC740D6DAD CRC64;  
 Query Match 57.7%; Score 45; DB 1; Length 260;  
 Best Local Similarity 53.3%; Pred. No. 1.4;  
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 Oy 1 MRYRASALGSDGVRV 15  
 Db 170 VRYMASSLGENIRV 184  
 RESULT 4  
 FABI\_ANASP  
 ID FABI\_ANASP STANDARD; PRT; 258 AA.  
 AC Q05069;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Enoyl-[acyl-carrier-protein] reductase [NADH] (EC 1.3.1.9) (NADH-  
 DE dependent enoyl-ACP reductase).  
 GN FABI OR ALA4391.  
 OS Anabaena sp. (strain PCC 7120).  
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
 OX NCBI\_TaxID=103690;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93308081; PubMed=8391534;  
 RA Wei T.-F., Ramasubramanian T.S., Pu F., Golden J.W.;  
 RT "Anabaena sp. strain PCC 7120 b1fa gene encoding a sequence-specific  
 RT DNA-binding protein cloned by in vivo transcriptional interference  
 RT selection.";  
 RL J. Bacteriol. 175:4025-4035(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21595285; PubMed=11759840;  
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,  
 RA Watanabe A., Iritguchi M., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
 RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,  
 RA Yasuda M., Tabata S.;  
 RT "Complete genomic sequence of the filamentous nitrogen-fixing  
 RT cyanobacterium *Anabaena* sp. strain PCC 7120.";  
 RL DNA Res. 8:205-213(2001).  
 CC -1- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + NAD(+) = trans-  
 CC 2,3-dehydroacyl-[acyl-carrier protein] + NADH.  
 CC -1- PATHWAY: SECOND REDUCTIVE STEP IN FATTY ACID BIOSYNTHESIS.  
 CC -1- SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN  
 CC DEHYDROGENASES/REDUCTASES (SDR) FAMILY.  
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DR EMBL: L10036; AAD04184.1; ALT\_INIT.  
 DR EMBL: AP003596; BAB76090.1; ALT\_INIT.  
 DR HSSP: P29132; 1DPI.  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short.1.  
 DR Oxidoreductase; NAD; Fatty acid biosynthesis; Complete proteome.  
 KW NP\_BIND 10 36 NAD (BY SIMILARITY).  
 FT SEQUENCE 258 AA; 27421 MW; 45012CA8497E001B CRC64;

Query Match 56.4%; Score 44; DB 1; Length 258;  
 Best Local Similarity 60.0%; Pred. No. 2.1;  
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MRYRASALSGDGVY 15  
 :|||:|||||:  
 Db 172 VRYLASELGSQNIYV 186

RESULT 5  
 ID FABI\_PSEAE STANDARD; PRT; 265 AA.  
 AC 093FEA;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Enoyl-[Acyl-carrier-protein] reductase [NADH] (EC 1.3.1.9) (NADH-  
 DE dependent enoyl-ACP reductase).  
 GN FABI OR PA1806  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 OC Pseudomonas.  
 OX NCBI\_TaxID=287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 15692 / PA01;  
 RX MEDLINE=9395061; Pubmed=10464225;  
 RA Hoang T.T., Schweizer H.P.;  
 RT "Characterization of Pseudomonas aeruginosa enoyl-acyl carrier protein  
 RT reductase (FabiI): a target for the antimicrobial triclosan and its  
 RT role in acylated homoserine lactone synthesis.";  
 RL J. Bacteriol. 181:5489-5497 (1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 15692 / PA01;  
 RX MEDLINE=20437337; Pubmed=10984043;  
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
 RA Hickey M.J., Brinkman F.S.L., Hutnagle W.O., Kowalik D.J., Lagrou M.,  
 RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,  
 RA Brody L.A., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
 RA Smith K.L., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 RA Reizer J., Seier M.H., Hancock R.E.W., Lory S., Olson M.V.;  
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an  
 RT opportunistic pathogen.";  
 RL Nature 406:959-964 (2000).  
 CC -1- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + NAD(+) = trans-  
 CC 2,3-dehydroacyl-[acyl-carrier protein] + NADH.  
 CC -1- PATHWAY: SECOND REDUCTIVE STEP IN FATTY ACID BIOSYNTHESIS.  
 CC -1- SUBCELLULAR LOCATION: Inner membrane-associated (By similarity).  
 CC -1- SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN  
 CC DEHYDROGENASES/REDUCTASES (SDR) FAMILY.  
 CC -----  
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DR EMBL: AF104262; AAC95362.1; -  
 DR EMBL: AE004607; AAC05195.1; -  
 DR HSSP: P29132; 1DPI.  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short.1.  
 DR Oxidoreductase; NAD; Fatty acid biosynthesis; Inner membrane;  
 KW Complete proteome.  
 FT NP\_BIND 10 36 NAD (BY SIMILARITY).  
 FT SEQUENCE 265 AA; 28006 MW; 3E7A946886DF293 CRC64;

Query Match 56.4%; Score 44; DB 1; Length 265;  
 Best Local Similarity 53.3%; Pred. No. 2.2;  
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRYRASALSGDGVY 15  
 :|||:|||||:  
 Db 173 VRYLACSLGAEQTRV 187

RESULT 6  
 ID YLDS\_CAEEL STANDARD; PRT; 1391 AA.  
 AC 003570; P39218; P34581;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical protein C38C10.5 in chromosome III.  
 GN C38C10.5.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2.  
 RX MEDLINE=94150718; Pubmed=7906398;  
 RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,  
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,  
 RA Fullon L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,  
 RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,  
 RA Lattrell P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,  
 RA Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R.,  
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,  
 RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,  
 RA Wohldman P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RT elegans.";  
 RL Nature 368:32-38 (1994).  
 RN [2]  
 RP REVISIONS, AND ALTERNATIVE SPLICING.  
 RA Jones S.J.M.;  
 RT Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; a and b (shown here); may be  
 CC produced by alternative splicing.  
 CC -1- SIMILARITY: TO YEAST RGT1.  
 CC -----  
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DR EMBL: Z29115; CAA82365.1; -  
 DR EMBL: Z19153; CAA82365.1; JOINED.  
 DR EMBL: Z19153; CAA9550.1; -  
 DR EMBL: Z29115; CAA9550.1; JOINED.  
 DR EMBL: Z29115; CAA82366.1; -

DR EMBL: Z19153; CAA82366.1; JOINED.  
 DR EMBL: Z19153; CAA79551.1; -  
 DR EMBL: Z29115; CAA79551.1; JOINED.  
 DR PIR: S28289; S28289.  
 DR Wormpep: C38c10.5; CE20550.  
 KM Hypothetical protein; Alternative splicing.  
 FT VASPLIC 671 676 MISSING (IN ISOFORM A).  
 SQ SEQUENCE 1391 AA: 157165 MW: 8702092D4C55A4BF CRC64;  
 Query Match 56.4%; Score 44; DB 1; Length 1391;  
 Best Local Similarity 50.0%; Pred. NO. 13;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 MRYRASALGSDGVRV 16  
 Db 1040 IFRRASQMGNGGVNAT 1055  
 RESULT 7  
 AMT4\_PSEST STANDARD; PRT; 548 AA.  
 ID AMT4\_PSEST  
 AC P13507;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Glucan 1,4-alpha-maltotetrahydrolase precursor (EC 3.2.1.60) (G4-  
 amyase) (Maltotetraose-forming amyase) (Exo-maltotetrahydrolase)  
 DE (Maltotetraose-forming exo-amyase).  
 GN AMP.  
 OS Pseudomonas stutzeri (Pseudomonas perfectomarina).  
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 OC Pseudomonas.  
 OX NCBI\_TaxID=316;  
 RN 11  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC STRAIN=MO-19;  
 RX MEDLINE=89155431; PubMed=2646279;  
 RA Fujita M., ToriGo K., Nakada T., Tsusaki K., Kubota M., Sakai S.,  
 RA Tsujioka Y.;  
 RT "Cloning and nucleotide sequence of the gene (ampy) for  
 RT maltotetraose-forming amyase from Pseudomonas stutzeri MO-19.";  
 RL J. Bacteriol. 171:1333-1339(1989).  
 RN 12  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS), AND REVISIONS TO 286-302.  
 RC STRAIN=MO-19;  
 RX MEDLINE=97271999; PubMed=9126844;  
 RA Morishita Y., Hasegawa K., Matsuura Y., Katsube Y., Kubota M.,  
 RA Sakai S.;  
 RT "Crystal structure of a maltotetraose-forming exo-amyase from  
 RT Pseudomonas stutzeri.";  
 RL J. Mol. Biol. 267:661-672(1997).  
 RN 13  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF VARIANT GLN-240.  
 RC STRAIN=MO-19;  
 RX MEDLINE=97428332; PubMed=9281429;  
 RA Yoshida Y., Hasegawa K., Matsuura Y., Katsube Y., Kubota M.;  
 RT "Crystal structures of a mutant maltotetraose-forming exo-amyase  
 RT co-crystallized with maltotetraose.";  
 RL J. Mol. Biol. 271:619-628(1997).  
 RN 14  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF VARIANTS.  
 RC STRAIN=MO-19;  
 RX MEDLINE=20027472; PubMed=10556241;  
 RA Hasegawa K., Kubota M., Matsuura Y.;  
 RT "Roles of catalytic residues in alpha-amyases as evidenced by the  
 RT structures of the product-complexed mutants of a maltotetraose-forming  
 RT amyase.";  
 RL Protein Eng. 12:819-824(1999).  
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages  
 CC in amyloseous polysaccharides so as to remove successive  
 CC maltotetraose residues from the non-reducing chain ends.  
 CC -1- COFACTOR: BINDS TWO CALCIUM IONS.  
 CC -1- PATHWAY: Starch degradation.

CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- MISCELLANEOUS: THERE ARE SEVERAL ISOENZYME FORMS OF THIS PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO  
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.  
 CC  
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 CC  
 DR EMBL: M24516; AAA25707.1; -  
 DR PIR: A32803; A32803.  
 DR PDB: 2AMG; 01-APR-97.  
 DR PDB: 1JDA; 15-OCT-97.  
 DR PDB: 1JDC; 15-OCT-97.  
 DR PDB: 1JDD; 15-OCT-97.  
 DR PDB: 1OI3; 24-NOV-99.  
 DR PDB: 1OI4; 24-NOV-99.  
 DR PDB: 1OI5; 24-NOV-99.  
 DR PDB: 1OPK; 17-NOV-99.  
 DR InterPro: IPR000461; Alpha-amyase.  
 DR InterPro: IPR002044; CBD\_4.  
 DR Pfam: PF00686; CBM\_20; 1.  
 DR Pfam: PD001568; CBD\_4; 1.  
 DR Prodom: PD001568; CBD\_4; 1.  
 KW Hydrolyase; Glycosidase; signal; Carbohydrate metabolism; Calcium;  
 KW 3D-structure.  
 FT SIGNAL 1 21  
 FT CHAIN 22 548 GLUCAN 1,4-ALPHA-MALTOSE HYDROLASE.  
 FT DISULFID 161 171  
 FT DISULFID 237 272  
 FT CA\_BIND 22 22 2.  
 FT CA\_BIND 23 23 2.  
 FT CA\_BIND 34 34 2.  
 FT CA\_BIND 37 37 2.  
 FT CA\_BIND 38 38 2.  
 FT CA\_BIND 137 137 1.  
 FT CA\_BIND 172 172 1.  
 FT CA\_BIND 175 175 1.  
 FT CA\_BIND 183 183 1.  
 FT ACT\_SITE 214 214 1.  
 FT ACT\_SITE 240 240  
 FT ACT\_SITE 315 315  
 FT CONFLICT 286 302  
 SQ SEQUENCE 548 AA: 59876 MW: 2887217B3379158F CRC64;  
 REF. 1)  
 Query Match 52.6%; Score 41; DB 1; Length 548;  
 Best Local Similarity 60.0%; Pred. NO. 16;  
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MRYRASALGSDGVRV 15  
 Db 116 LRQASALGAGGVK 130  
 RESULT 8  
 FA12\_RHIME STANDARD; PRT; 268 AA.  
 ID FA12\_RHIME  
 AC P58381;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Enoyl-lacyl-carrier-protein) reductase [NADH] 2 (EC 1.3.1.9) (NADH-  
 DE dependent enoyl-ACP reductase 2).  
 GN FAB12 OR R00246 OR SMC00326  
 OS Rhizobium meliloti (Sinorhizobium meliloti).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Sinorhizobium.  
 OX NCBI\_TaxID=382;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021:
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Drenth S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetleau D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
CC -1- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + NAD(+) = trans-
CC 2,3-dehydroacyl-[acyl-carrier protein] + NADH.
CC -1- PATHWAY: SECOND REDUCTIVE STEP IN FATY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: Inner membrane-associated (By similarity).
CC -1- SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN
CC DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
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CC -----
DR EMBL: AL591783; CAC41683.1; -.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR Oxidoreductase; NAD; Fatty acid biosynthesis; Inner membrane;
KW Complete proteome.
FT NP_BIND 11 37 NAD (BY SIMILARITY).
SQ SEQUENCE 268 AA; 26671 MW; 83D2127C7D76628C CRC64;

Query Match 50.0%; Score 39; DB 1; Length 268;
Best Local Similarity 53.3%; Pred. No. 16;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MRYRASALGSDGVRY 15
DB 170 VRYLADYGSRGIRV 184

RESULT 9
RLAL_MAIZE STANDARD; PRT; 109 AA.
AC P52855; O24414;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 60S acidic ribosomal protein P1 (L12).
GN RPLP1A.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. W22;
RA Hamilton D.A., Turcich M.P., Bokhari-Riza A., Mascarenhas J.P.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-21.
RC STRAIN=cv. B73; TISSUE=Ear;
RX MEDLINE=97422884; PubMed=9276949;
RA Bailey-Serres J., Vangala S., Szick K., Lee C.H.;
RT "Acidic phosphoprotein complex of the 60S ribosomal subunit of maize
RT seedling roots. Components and changes in response to flooding."
RL Plant Physiol. 114:1293-1305(1997).
CC -1- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE ELONGATION STEP OF
CC PROTEIN SYNTHESIS (BY SIMILARITY).

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CC -1- SUBUNIT: P1 AND P2 EXIST AS DIMERS AT THE LARGE RIBOSOMAL
CC SUBUNIT (BY SIMILARITY).
CC -1- PTM: PHOSPHORYLATED.
CC -1- PTM: THE N-TERMINUS IS BLOCKED.
CC -1- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.
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CC -----
DR EMBL: U04147; AAA91168.1; -.
DR EMBL: U62752; AAB71079.1; -.
DR MaizEDB: 84941; -.
DR InterPro: IPR001813; 60S_ribosomal.
DR Pfam: PF00428; 60S_ribosomal; 1.
DR Ribosomal protein.
KW CONFLICT 9 9 R -> T (IN REF. 2).
FT CONFLICT 9 9
SQ SEQUENCE 109 AA; 11096 MW; 1BFECE8E34391F080 CRC64;

Query Match 48.7%; Score 38; DB 1; Length 109;
Best Local Similarity 46.7%; Pred. No. 9;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 RYRASALGSDGVRY 16
DB 9 RYALALLSDGIAIT 23

RESULT 10
CYSC_ARCFU STANDARD; PRT; 155 AA.
ID CYSC_ARCFU
AC Q29953;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable adenylylsulfate kinase (EC 2.7.1.25) (APS kinase) (Adenosine-
DE 5'-phosphosulfate kinase) (ATP adenosine-5'-phosphosulfate 3'-
DE phosphotransferase).
GN CYSC OR AF0288.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kierlavage A.R., Graham D.E., Kyrides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Uitterlisch T.,
RA Cotton M.D., Spriggs T., Artiach P., Kalne B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus."
RL Nature 390:364-370(1997).
CC -1- FUNCTION: CATALYZES THE SYNTHESIS OF ACTIVATED SULFATE.
CC -1- CATALYTIC ACTIVITY: ATP + adenylylsulfate = ADP + 3'-
CC 5'-phosphadenylylsulfate.
CC -1- PATHWAY: SECOND STEP IN THE SULFATE ACTIVATION PATHWAY. INVOLVED
CC IN THE ENERGY-GENERATING SULFUR OXIDATION PATHWAYS OF MANY
CC CHEMOAUTOTROPHIC MICROBES.
CC -1- SIMILARITY: BELONGS TO THE APS KINASE FAMILY.
CC -----

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DR EMBL: AE001085; AAB90945.1; -  
 DR TIGR: AF0288; -  
 DR InterPro: IPR002891; APS\_kinase.  
 DR Pfam: PF01583; APS\_kinase; 1.  
 DR ProDom: PD002350; APS\_kinase; 1.  
 DR TrnRFams: TIGR00455; apsk; 1.  
 KW Transferrase; kinase; ATP-binding; Phosphorylation; Complete proteome.  
 FT NP\_BIND 9 16 ATP (BY SIMILARITY)  
 FT ACT\_SITE 83 83 FORMS THE PHOSPHOSERINE INTERMEDIATE (BY  
 FT SIMILARITY).  
 SQ SEQUENCE 155 AA; 17893 MW; 4535298F48931881 CRC64;

Query Match 48.7%; Score 38; DB 1; Length 155;  
 Best Local Similarity 57.1%; Pred. No. 13;  
 Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 MRRASALGSDGVR 14  
 Db 29 MGYRVELLDGQVR 42

RESULT 11  
 TPIS\_SULTO  
 ID PPIS\_SULTO STANDARD; PRT; 229 AA.  
 AC 096129;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Triosephosphate isomerase (EC 5.3.1.1) (TIM).  
 GN TPISA OR ST2030.  
 OS Sulfolobus tokodaii.  
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;  
 OC Sulfolobus.  
 OX NCBI\_TaxID=111955;  
 (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TCM 10545 / 7;  
 RX MEDLINE=21456156; Pubmed=11572479;  
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takehashi M.,  
 RA Sekine M., Baba S.-I., Ankaï A., Kosugi H., Hosoyama A., Fukui S.,  
 RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,  
 RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,  
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,  
 RA Oshima T., Kikuchi H.;  
 RT "Complete genome sequence of an aerobic thermophilic  
 RT Crenarchaeon, Sulfolobus tokodaii strain 7."  
 RT DNA Res. 8:123-140(2001).  
 CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycero-  
 CC phosphate.  
 CC -1- PATHWAY: Plays an important role in several metabolic pathways.  
 CC -1- SUBUNIT: Homotrimer (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.  
 CC -----  
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DR EMBL: AP000988; BAB67127.1; -  
 DR InterPro: IPR003009; FMN\_enzyme.  
 DR InterPro: IPR000652; Trlphos\_ismrse.  
 DR ProDom: PD001005; Trlphos\_ismrse; 1.

DR TIGRFams: TIGR00419; tlm; 1.  
 DR PROSITE: PS00171; TIM; FALSE\_NEG.  
 KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;  
 KW Pentose shunt; Complete proteome.  
 FT ACT\_SITE 93 93 BY SIMILARITY  
 SQ SEQUENCE 229 AA; 24898 MW; 9DC1D550A01B5525 CRC64;

Query Match 48.7%; Score 38; DB 1; Length 229;  
 Best Local Similarity 53.8%; Pred. No. 20;  
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 YRASALGSDGVR 15  
 Db 188 YKAIELGADGIV 200

RESULT 12  
 FAL1\_RHIME  
 ID FAL1\_RHIME STANDARD; PRT; 272 AA.  
 AC P58380;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Enoyl-[acyl-carrier-protein] reductase [NADH] 1 (EC 1.3.1.9) (NADH-  
 DE dependent enoyl-ACP reductase 1).  
 GN FABL1 OR R00898 OR SMC00005.  
 OS Rhizobium meliloti (Sinorhizobium meliloti).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Sinorhizobium.  
 OX NCBI\_TaxID=382;  
 (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1021;  
 RX MEDLINE=21396507; Pubmed=11481430;  
 RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,  
 RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,  
 RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaire V., Masuy D.,  
 RA Pohl T., Portetle D., Puehler A., Purnelle B., Ransperger U.,  
 RA Renard C., Thebaud P., Vandendol M., Weidner S., Gallibert F.;  
 RT "Analysis of the chromosome sequence of the legume symbiont  
 RT Sinorhizobium meliloti strain 1021."  
 RT Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).  
 CC -1- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + NADH.  
 CC 2,3-dehydroacyl-[acyl-carrier protein] + NADH.  
 CC -1- PATHWAY: SECOND REDUCTIVE STEP IN FATTY ACID BIOSYNTHESIS.  
 CC -1- SUBCELLULAR LOCATION: Inner membrane-associated (By similarity).  
 CC -1- SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN  
 CC DEHYDROGENASES/REDUCTASES (SDR) FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: AL591785; CAC45470.1; -  
 DR InterPro: IPR002198; ADH\_short.  
 DR Pfam: PF00106; adh\_short; 1.  
 KW Oxidoreductase; NAD; Fatty acid biosynthesis; Inner membrane;  
 FT NP\_BIND 14 40 NAD (BY SIMILARITY).  
 SQ SEQUENCE 272 AA; 29148 MW; 1E0F1A8A22CDBE36 CRC64;

Query Match 48.7%; Score 38; DB 1; Length 272;  
 Best Local Similarity 53.3%; Pred. No. 24;  
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 MRRASALGSDGVR 15  
 Db 173 VRYLVLDLGNRGIR 187

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RESULT 13
GSA_CAMJG STANDARD: PRT: 424 AA.
ID GSA_CAMJG
AC 09PT70.
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) (GSA)
DE (Glutamate-1-semialdehyde aminotransferase) (GSA-AT).
CN HEML OR C30853.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NCCTC 11168;
RX MEDLINE=20150912; PubMed=10689204;
RA Parhill J., Wren B.W., Mungall K.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrett B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences."
RL Nature 403:665-668(2000).
CC -1- CATALYTIC ACTIVITY: (S)-4-amino-5-oxopentanoate = 5-
CC aminovalerate.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- PATHWAY: porphyrin biosynthesis by the C5 pathway; second step.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AL139076; CAB73118.1; -.
CC HSSP: P24630; 2GSA.
CC InterPro: IPR000954; AminoTran_3.
CC DR InterPro: IPR004639; HemL.
CC DR Pfam: PF00202; aminoTran_3; 1.
CC DR TIGRfams: TIGR00713; hemL; 1.
CC DR PROSITE: PS00600; AA_TRANSFERS_CLASS_3; FALSE NEG.
CC K01 Porphyrin biosynthesis; isomerase; Pyridoxal phosphate;
CC KW Complete proteome. 263 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC FT BINDING 263
CC SEQUENCE 424 AA; 46092 MW; 7811526A5AD57D CRC64;
Query Match 48.7%; Score 38; DB 1; Length 424;
Best Local Similarity 72.7%; Pred. No. 39;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 3 YRASALGSDGV 13
DB 241 YRASLGSYGI 251
RESULT 14
CYAE_BORPE STANDARD: PRT: 474 AA.
ID CYAE_BORPE
AC P11092;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein cyae precursor.

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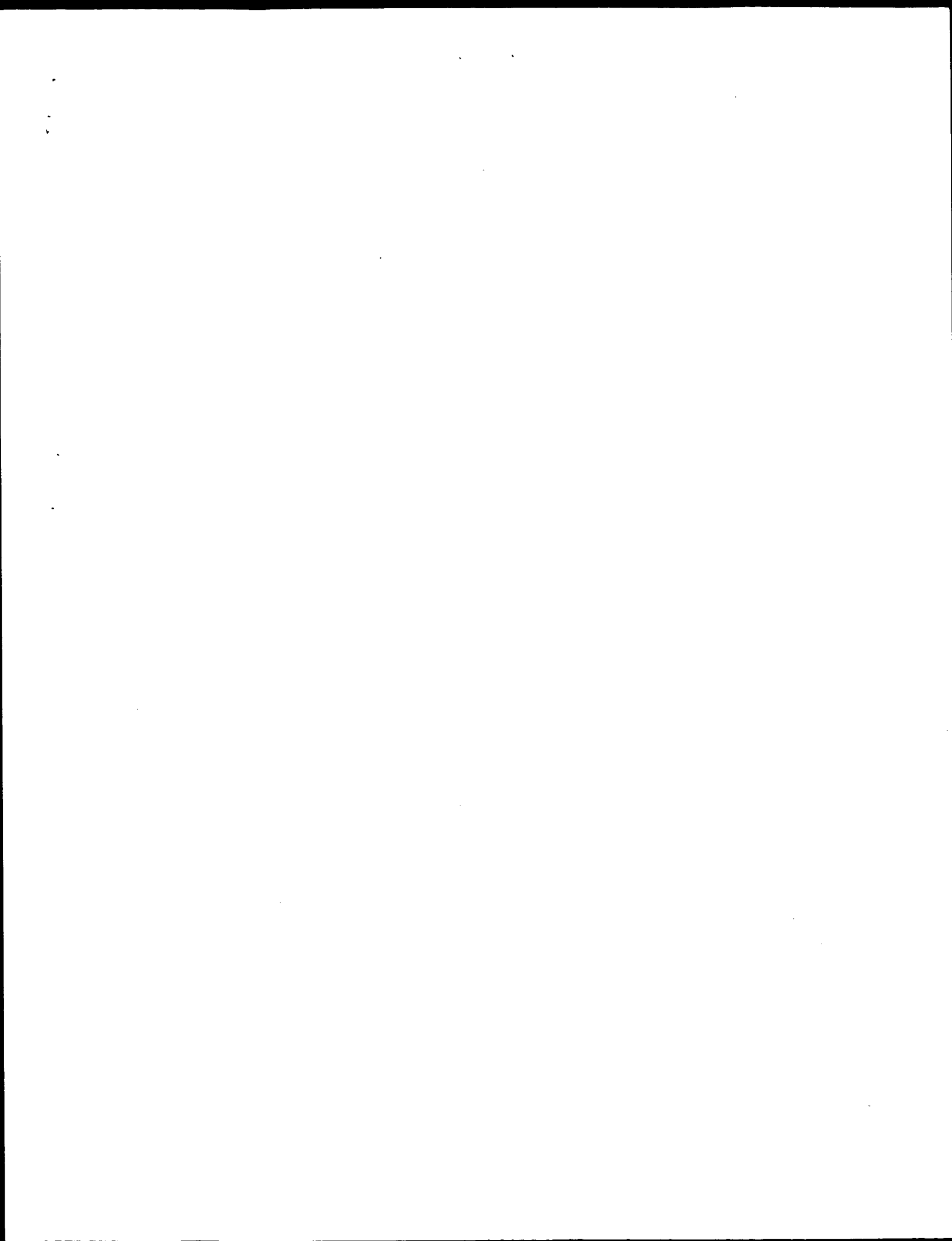
GN CYAE.
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
OC Bordetella.
OX NCBI_TaxID=520;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=18323;
RX MEDLINE=89091151; PubMed=2905265;
RA Glaser P., Sakamoto H., Bellalou J., Ullmann A., Danchin A.;
RT "Secretion of cyclolysin, the calmodulin-sensitive adenylate cyclase-
RT haemolysin bifunctional protein of Bordetella pertussis."
RL EMBL J. 7:3997-4004(1988).
CC -1- FUNCTION: CYAE IS NECESSARY FOR TRANSPORT OF CALMODULIN-SENSITIVE
CC ADENYLATE CYCLASE-HEMOLYSIN (CYCLOLYSIN).
CC -1- SUBCELLULAR LOCATION: Outer membrane (By similarity).
CC -1- SIMILARITY: BELONGS TO THE PRTF FAMILY OF SECRETION PROTEINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X14199; CAA32414.1; -.
CC PIR: S02388; BVRCE.
CC InterPro: IPR003423; OEP.
CC DR Pfam: PF02321; OEP; 2.
CC DR Hemolysin; Transpor; Outer membrane; Signal.
CC KW Hemolysin; 1 POTENTIAL.
CC FT SIGNAL 31
CC CHAIN 32 474 PROTEIN CYAE.
CC SEQUENCE 474 AA; 50204 MW; 29A4F21D377FC957 CRC64;
Query Match 48.7%; Score 38; DB 1; Length 474;
Best Local Similarity 63.6%; Pred. No. 44;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 4 RASALGSDGVR 14
DB 115 RSTGLGSDGVR 125
RESULT 15
YMA6_MYCTU STANDARD: PRT: 513 AA.
ID YMA6_MYCTU
AC Q10510;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein RV2226.
DE RV2226 OR MT2285 OR MYC9427.07.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holtroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RT Nature 393:537-544(1998).
RN [2]

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RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / Oshkosh;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,  
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
 RA Bishai W.;  
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 laboratory strains."  
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.  
 CC -----  
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 CC -----  
 CC EMBL: Z70692; CAA94649.1; -;  
 DR EMBL: AE007073; AAK46570.1; -;  
 DR TIGR: MT2285; -;  
 DR TubercuList: RV2226; -;  
 KW Hypothetical protein; Complete proteome.  
 FT CONFLICT 289 D -> N (IN REF. 2).  
 SQ SEQUENCE 513 AA: 56333 MW: 8E74BDA8945D7B99 CRC64;

Query Match 48.7%; Score 38; DB 1; Length 513;  
 Best Local Similarity 53.8%; Pred. No. 48;  
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MRYRASALGSDGV 13  
 : 1 1 1 1 1 1 1  
 DB 426 LRYTAATGADNV 438

Search completed: January 16, 2003, 10:12:28  
 Job time : 12 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 16, 2003, 10:11:32 ; Search time 14 Seconds  
(without alignments)  
33.626 Million cell updates/sec

Title: US-09-893-371-2

Perfect score: 78  
Sequence: 1 MRYRASALGSDGVRYT 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCITUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	62.8	262	1	US-08-241-766-8
2	49	62.8	262	1	US-08-241-766-9
3	38	48.7	308	4	US-09-347-803-12
4	38	48.7	985	5	PCIT-US96-03916-6
5	38	48.7	985	5	PCIT-US96-03916-6
6	37	47.4	309	4	US-09-134-001C-3039
7	37	47.4	623	3	US-09-041-991A-6
8	37	47.4	943	4	US-09-134-001C-4009
9	36	46.2	260	4	US-09-397-885-5
10	36	46.2	537	1	US-08-173-508-2
11	36	46.2	537	1	US-08-265-310-2
12	36	46.2	537	3	US-08-951-742-2
13	36	46.2	635	3	US-09-041-991A-4
14	36	46.2	702	6	5240838-15
15	36	46.2	3729	2	US-08-804-227C-4
16	35	44.9	48	2	US-08-637-759B-480
17	35	44.9	48	3	US-08-871-355A-480
18	35	44.9	48	4	US-09-201-945-480
19	35	44.9	256	4	US-09-292-412-2
20	35	44.9	303	4	US-09-420-786A-3
21	35	44.9	308	4	US-09-347-803-10
22	35	44.9	338	4	US-09-199-637A-47
23	35	44.9	350	4	US-08-961-083-126
24	35	44.9	5588	4	US-09-036-987A-6
25	35	44.9	5588	4	US-09-370-700-6
26	34	43.6	77	4	US-09-465-558-52
27	34	43.6	113	1	US-08-211-202-114

28	34	43.6	303	2	US-08-286-819A-23	Sequence 23, Appl
29	34	43.6	303	3	US-08-980-357-23	Sequence 23, Appl
30	34	43.6	319	2	US-08-795-927-4	Sequence 4, Appl
31	34	43.6	329	3	US-09-022-669-2	Sequence 2, Appl
32	34	43.6	329	4	US-09-262-749-2	Sequence 2, Appl
33	34	43.6	329	4	US-09-603-567-2	Sequence 2, Appl
34	34	43.6	359	4	US-09-722-139-4	Sequence 4, Appl
35	34	43.6	359	4	US-09-721-832-4	Sequence 4, Appl
36	34	43.6	359	4	US-09-721-832-4	Sequence 4, Appl
37	34	43.6	433	4	US-09-199-637A-349	Sequence 349, App
38	34	43.6	524	4	US-08-529-654-4	Sequence 4, Appl
39	34	43.6	524	3	US-08-957-302A-2	Sequence 2, Appl
40	34	43.6	524	4	US-09-542-403-2	Sequence 2, Appl
41	34	43.6	524	4	US-09-042-709A-20	Sequence 20, Appl
42	34	43.6	623	1	US-08-653-740-7	Sequence 7, Appl
43	34	43.6	623	2	US-09-073-594-7	Sequence 7, Appl
44	34	43.6	623	3	US-09-275-925-7	Sequence 7, Appl
45	34	43.6	633	3	US-09-041-991A-8	Sequence 8, Appl

#### ALIGNMENTS

RESULT 1  
US-08-241-766-8  
Sequence 8, Application US/08241766

Patent No. 5685590

GENERAL INFORMATION:

APPLICANT: JACOBS, W. R.

APPLICANT: COLLINS, D. M.

APPLICANT: BANERJEE, A. M.

APPLICANT: DELISTE, G. W.

APPLICANT: WILSON, T. M.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING

TITLE OF INVENTION: AND TREATING MYCOBACTERIAL INFECTIONS USING AN INHA AGENT

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/241,766

FILING DATE: 12-MAY-1994

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: MONROY, GLADYS H.

REGISTRATION NUMBER: 32,430

REFERENCE/DOCKET NUMBER: 25237-20003.20

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 262 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-241-766-8

Query Match

Best Local Similarity 62.8%; Score 49; DB 1; Length 262;

Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

1 MRYRASALGSDGVRY 15

Db 170 VRYMANMGPEGVRY 184

# RESULT 2

US-08-241-766-9  
 ; Sequence 9, Application US/08241766  
 ; Patent No. 5686590  
 ; GENERAL INFORMATION:  
 ; APPLICANT: JACOBS, W. R.  
 ; APPLICANT: COLLINS, D. M.  
 ; APPLICANT: BANERJEE, A.  
 ; APPLICANT: DELISLE, G. W.  
 ; APPLICANT: WILSON, T. M.  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING  
 ; TITLE OF INVENTION: AND TREATING MYCOBACTERIAL INFECTIONS USING AN LHA AGENT  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: MORRISON & FOERSTER  
 ; STREET: 755 Page Mill Road  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94304-1018  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/241,766  
 ; FILING DATE: 12-MAY-1994  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: MONROY, GLADYS H.  
 ; REGISTRATION NUMBER: 32,430  
 ; REFERENCE/DOCKET NUMBER: 25237-20003.20  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 813-5600  
 ; TELEFAX: (415) 494-0792  
 ; TELEX: 706141  
 ; INFORMATION FOR SEQ ID NO: 9:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 262 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-241-766-9

Query Match 62.8%; Score 49; DB 1; Length 262;  
 Best Local Similarity 60.08; Pred. No. 0.51;  
 Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 MRYASALGSDGVRY 15  
 Db 170 VRYMANMGPEGVRY 184

# RESULT 3

US-09-347-803-12  
 ; Sequence 12, Application US/09347803  
 ; Patent No. 6274379  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Famodu, Layo O.  
 ; APPLICANT: Hitz, Bill  
 ; APPLICANT: Kinney, Tony  
 ; APPLICANT: Orozco, Buddy  
 ; TITLE OF INVENTION: Plant Sorbitol Biosynthetic Enzymes  
 ; FILE REFERENCE: BB-1176  
 ; CURRENT APPLICATION NUMBER: US/09/347,803  
 ; CURRENT FILING DATE: 1999-07-02  
 ; EARLIER APPLICATION NUMBER: 60/092,952  
 ; EARLIER FILING DATE: July 15, 1998

NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: Microsoft Office 97  
 ; SEQ ID NO 12  
 ; LENGTH: 308  
 ; TYPE: PRT  
 ; ORGANISM: Oryza sativa  
 ; US-09-347-803-12

Query Match 48.7%; Score 38; DB 4; Length 308;  
 Best Local Similarity 88.9%; Pred. No. 48;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 ASALGSDGV 13  
 Db 120 ASALGDCGV 128

# RESULT 4

PCT-US96-03916-6  
 ; Sequence 6, Application PC/TUS9603916  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wild, Martha A.  
 ; APPLICANT: Cochran, Mark D.  
 ; TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS  
 ; TITLE OF INVENTION: AND USES THEREOF  
 ; NUMBER OF SEQUENCES: 72  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooper & Dunham LLP  
 ; STREET: 1185 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US96/03916  
 ; FILING DATE: 23-MAR-1995  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/126,597  
 ; FILING DATE: 24-SEP-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: White, John P.  
 ; REGISTRATION NUMBER: 28,678  
 ; REFERENCE/DOCKET NUMBER: 39116-A  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 278-0400  
 ; TELEFAX: (212) 391-0525  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 985 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: Protein  
 ; PCT-US96-03916-6

Query Match 48.7%; Score 38; DB 5; Length 985;  
 Best Local Similarity 57.1%; Pred. No. 1.7e+02;  
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 3 YRASALGSDGVRY 16  
 Db 921 YECTVLISDSTRVT 934

# RESULT 5

PCT-US96-03916-66  
 ; Sequence 66, Application PC/TUS9603916  
 ; GENERAL INFORMATION:

APPLICANT: Wild, Martha A.  
APPLICANT: Cochran, Mark D.  
TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS  
TITLE OF INVENTION: AND USES THEREOF  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/03916  
FILING DATE: 23-MAR-1995  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/126,597  
FILING DATE: 24-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 39116-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 985 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-03916-66

Query Match 48.7% Score 38; DB 5; Length 985;  
Best Local Similarity 57.1% Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 YRASALGSDGVRVT 16  
DB 922 YECTVLISDGTIRVT 934

RESULT 6  
US-09-134-001C-3039  
Sequence 3039, Application US/09134001C  
Patent No. 6380370  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GTC-007  
CURRENT APPLICATION NUMBER: US/09/134,001C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/064,964  
PRIOR FILING DATE: 1997-11-08  
PRIOR APPLICATION NUMBER: US 60/055,779  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 5674  
SEQ ID NO 3039  
LENGTH: 309  
TYPE: PRT  
ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3039

Query Match 47.4% Score 37; DB 4; Length 309;  
Best Local Similarity 50.0% Pred. No. 71;  
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 RYRASALGSDGVRV 15  
DB 272 RYEHRLGIDPVKL 285

RESULT 7  
US-09-041-991A-6  
Sequence 6, Application US/09041991A  
Patent No. 6107278  
GENERAL INFORMATION:  
APPLICANT: Schnepf, H. Ernest  
APPLICANT: Narva, Kenneth E.  
APPLICANT: Muller-Cohn, Judy  
TITLE OF INVENTION: Toxins Active Against Pests  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentlin  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/041,991A  
FILING DATE: 13-MAR-1998  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: MA-709  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 623 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-041-991A-6

Query Match 47.4% Score 37; DB 3; Length 623;  
Best Local Similarity 53.8% Pred. No. 1.5e+02;  
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 RASALGSDGVRVT 16  
DB 539 RVSSIGSSTIRVT 551

RESULT 8  
US-09-397-885-5  
Sequence 5, Application US/09397885  
Patent No. 6323007  
GENERAL INFORMATION:  
APPLICANT: Moller, Soren  
APPLICANT: Johansen, Charlotte  
APPLICANT: Schaefer, Thomas  
APPLICANT: Ostergaard, Peter Rahbek  
APPLICANT: Hoeck, Lisbeth Hedegaard  
TITLE OF INVENTION: A 2,6,-b-D-fructan Hydrolase Enzyme And  
FILE REFERENCE: 5540.200-US  
CURRENT APPLICATION NUMBER: US/09/397,885  
CURRENT FILING DATE: 1999-09-17  
EARLIER APPLICATION NUMBER: PA 1998 01173

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; EARLIER FILING DATE: 1998-09-18
; EARLIER APPLICATION NUMBER: PA 1998 01623
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: 60/101,615
; EARLIER FILING DATE: 1998-09-24
; EARLIER APPLICATION NUMBER: 60/111,675
; EARLIER FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 5
; LENGTH: 943
; TYPE: PRT
; ORGANISM: paenibacillus macerans
; US-09-397-885-5

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Query Match          47.4%; Score 37; DB 4; Length 943;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MRYRASALGSDG 12
DB 270 LRRRANGCGTGD 281

```

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RESULT 9
US-09-134-001C-4009
; Sequence 4009, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lyon Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4009
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
; US-09-134-001C-4009

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Query Match          46.2%; Score 36; DB 4; Length 260;
Best Local Similarity 46.7%; Pred. No. 88;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

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QY 1 MRYRASALGSDGVRV 15
DB 175 VKYLALDGEDNIRV 189

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RESULT 10
US-08-173-508-2
; Sequence 2, Application US/08173508
; Patent No. 5616485
; GENERAL INFORMATION:
; APPLICANT: Bartfeld, Daniel
; APPLICANT: Butler, Michael J.
; APPLICANT: Hadary, Dany
; APPLICANT: Jenish, David
; APPLICANT: Krieger, Timothy
; TITLE OF INVENTION: STREPTOMYCES PROTEASES AND IMPROVED
; TITLE OF INVENTION: STREPTOMYCES STRAINS FOR EXPRESSION OF PEPTIDES AND
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W.
; CITY: Washington, D.C.

```

```

; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,508
; FILING DATE: 23-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 18740/125/CACO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 672 5300
; TELEFAX: 202 672 5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 537 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-173-508-2

```

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Query Match          46.2%; Score 36; DB 1; Length 537;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

```

```

QY 1 MRYRASALGSDGVRV 16
DB 6 IRRRAAFGTAGAVT 21

```

```

RESULT 11
US-08-265-310-2
; Sequence 2, Application US/08265310
; Patent No. 5856166
; GENERAL INFORMATION:
; APPLICANT: Bartfeld, Daniel
; APPLICANT: Butler, Michael J.
; APPLICANT: Hadary, Dany
; APPLICANT: Jenish, David
; APPLICANT: Krieger, Timothy
; APPLICANT: Malek, Lawrence T.
; APPLICANT: Soostmeyer, Gisela
; APPLICANT: Walczyk, Eva
; APPLICANT: Krysgman, Phyllis
; APPLICANT: Garven, Sheila
; TITLE OF INVENTION: STREPTOMYCES PROTEASES AND IMPROVED
; TITLE OF INVENTION: STREPTOMYCES STRAINS FOR EXPRESSION OF PEPTIDES AND
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,310
; FILING DATE: 24-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,508
; FILING DATE: 23-DEC-1993

```

ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 18740/133/CACO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202 672 5300  
TELEFAX: 202 672 5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 537 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-265-310-2

Query Match 46.2%; Score 36; DB 2; Length 537;  
Best Local Similarity 50.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MRYRASALGSDGVRYT 16  
Db 6 IRRRATAFGTAGALVT 21

RESULT 12  
US-08-951-742-2  
Sequence 2, Application US/08951742  
Patent No. 6127144  
GENERAL INFORMATION:  
APPLICANT: Bartfeld, Daniel  
APPLICANT: Michael J. Butler  
APPLICANT: Dany Hadary  
APPLICANT: David Jenish  
APPLICANT: Tim Krieger  
APPLICANT: Lawrence T. Malek  
APPLICANT: Gisela Soostmeyer  
APPLICANT: Eva Walczyk  
APPLICANT: Phyllis Krysgsmn  
APPLICANT: Sheila Garven  
TITLE OF INVENTION: METHOD FOR EXPRESSION OF PROTEINS IN  
TITLE OF INVENTION: BACTERIAL HOST CELLS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/951,742  
FILING DATE: 16-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Bent, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 0189740/0140  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 537 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-951-742-2

Query Match 46.2%; Score 36; DB 3; Length 537;  
Best Local Similarity 50.0%; Pred. No. 1.9e+02;  
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MRYRASALGSDGVRYT 16  
Db 6 IRRRATAFGTAGALVT 21

RESULT 13  
US-09-041-991A-4  
Sequence 4, Application US/09041991A  
Patent No. 6107278  
GENERAL INFORMATION:  
APPLICANT: Schnepf, H. Ernest  
APPLICANT: Narva, Kenneth E.  
APPLICANT: Muller-Cohn, Judy  
TITLE OF INVENTION: Toxins Active Against Pests  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanichik, Lloyd & Saliwanichik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/041,991A  
FILING DATE: 13-MAR-1998  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay M.  
REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: MA-709  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 635 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-041-991A-4

Query Match 46.2%; Score 36; DB 3; Length 635;  
Best Local Similarity 53.8%; Pred. No. 2.3e+02;  
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 RASALGSDGVRYT 16  
Db 550 RVSSLGNTIRVT 562

RESULT 14  
5240838-15  
Patent No. 5240838  
APPLICANT: LEDERER, ADRIANUS M.; MAAT, JAN; VERRIPS, CORNELIS  
T.; VISSER, CHRISTIAN; JONOWICZ, ZBIGNIEW A.; HOLLENBERG, CORNELIS P.  
TITLE OF INVENTION: REGULATORY SEQUENCES OF ALCOHOL OXIDASE  
(MOX) AND DIHYDROXYACETONESYNTHASE (DAS) OF HANSENULLA POLYMORPHA  
NUMBER OF SEQUENCES: 19  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/587,555  
FILING DATE: 24-SEP-1990  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 300,211  
FILING DATE: 23-JAN-1989  
APPLICATION NUMBER: 759,315  
FILING DATE: 26-JUL-1985  
SEQ ID NO: 15  
LENGTH: 702  
5240838-15

Query Match 46.2%; Score 36; DB 6; Length 702;  
Best Local Similarity 77.8%; Pred. No. 2.6e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 6 SAICSDGVR 14  
: ||| |||  
Db 277 NALGEDGVR 285

## RESULT 15

US-08-804-227C-4  
Sequence 4, Application US/08804227C  
Patent No. 5876991  
GENERAL INFORMATION:  
APPLICANT: Dehoff, Bradley S.  
APPLICANT: Kuhnstos, Stuart A.  
APPLICANT: Rosteck, Paul R., Jr.  
APPLICANT: Sutton, Kimberly L.  
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: THOMAS G. PLANT 1501  
STREET: LILLY CORPORATE CENTER  
CITY: INDIANAPOLIS  
STATE: IN  
COUNTRY: USA  
ZIP: 46285  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: ASCI(DOS) Text only  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/804,227C  
FILING DATE: February 21, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Plant, Thomas, G.  
REGISTRATION NUMBER: 35,784  
REFERENCE/DOCKET NUMBER: X-8231  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 317-276-2459  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3729 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-804-227C-4

Query Match 46.2%; Score 36; DB 2; Length 3729;  
Best Local Similarity 66.7%; Pred. No. 1.6e+03;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 RYRASALGSDGV 13  
: ||| |||  
Db 1778 RSRAPAGAGDV 1789

Search completed: January 16, 2003, 10:13:48  
Job time : 15 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 16, 2003, 10:13:13 ; Search time 11 Seconds  
(Without alignments)  
28.914 Million cell updates/sec

Title: US-09-893-371-2  
Perfect score: 78  
Sequence: 1 MRYRASALGSDGVKVT 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 120991 seqs, 19878514 residues

Total number of hits satisfying chosen parameters: 120991

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*

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2: /cgn2\_6/ptodata/2/pubppaa/PCY\_NEW\_PUB pep: \*  
3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB pep: \*  
4: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB pep: \*  
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10: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB pep: \*  
11: /cgn2\_6/ptodata/2/pubppaa/US10\_NEW\_PUB pep: \*  
12: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB pep: \*  
13: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB pep: \*  
14: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	62.8	262	10 US-09-815-242-10152	Sequence 10152, A
2	49	62.8	269	10 US-09-815-242-13824	Sequence 13824, A
3	44	56.4	265	10 US-09-815-242-11851	Sequence 11851, A
4	38	48.7	315	10 US-09-815-242-13289	Sequence 13289, A
5	38	48.7	1233	9 US-09-738-626-4312	Sequence 4312, Ap
6	37	47.4	441	9 US-09-738-626-4275	Sequence 4275, Ap
7	37	47.4	722	9 US-09-738-626-5453	Sequence 5453, Ap
8	37	47.4	943	10 US-09-969-362-5	Sequence 5
9	37	47.4	1316	9 US-10-120-544A-4	Sequence 4, Appl1
10	37	47.4	1344	9 US-10-120-544A-20	Sequence 20, Appl1
11	37	47.4	1386	9 US-10-120-544A-6	Sequence 6, Appl1
12	36	46.2	50	10 US-09-864-761-40694	Sequence 40694, A
13	36	46.2	295	10 US-09-815-242-11279	Sequence 11279, A
14	36	46.2	358	9 US-09-738-626-4829	Sequence 4829, Ap
15	35	46.2	1160	9 US-10-028-072-234	Sequence 234, App
16	35	44.9	256	10 US-09-815-242-5228	Sequence 5228, Ap
17	35	44.9	256	10 US-09-815-242-12535	Sequence 12535, A
18	35	44.9	256	10 US-09-815-242-12892	Sequence 12892, A
19	35	44.9	316	10 US-09-815-242-13929	Sequence 13929, A

20	35	44.9	350	10 US-09-765-272-126	Sequence 126, App
21	35	44.9	558	10 US-09-770-517C-2	Sequence 2, Appl1
22	34.5	44.2	94	9 US-09-976-059-29	Sequence 29, Appl1
23	34.5	44.2	666	10 US-09-815-242-1933	Sequence 4933, Ap
24	34.5	44.2	677	10 US-09-815-242-10663	Sequence 10663, A
25	34.5	44.2	3034	10 US-09-737-149-25	Sequence 25, Appl1
26	34.5	44.2	3034	10 US-09-737-149-30	Sequence 30, Appl1
27	34	43.6	220	10 US-09-815-242-13735	Sequence 13735, A
28	34	43.6	229	9 US-09-965-529-22	Sequence 22, Appl1
29	34	43.6	319	9 US-10-001-426-4	Sequence 4, Appl1
30	34	43.6	319	9 US-10-003-014-4	Sequence 4, Appl1
31	34	43.6	345	10 US-09-925-300-1188	Sequence 1188, Ap
32	34	43.6	423	9 US-09-911-317-4	Sequence 4, Appl1
33	34	43.6	513	10 US-09-833-745-46	Sequence 46, Appl1
34	34	43.6	810	9 US-09-712-363-281	Sequence 281, App
35	34	43.6	911	10 US-09-745-763-140	Sequence 140, App
36	34	43.6	1430	10 US-09-740-274-6	Sequence 6, Appl1
37	34	43.6	3739	9 US-09-860-846-33	Sequence 33, Appl1
38	34	43.6	3739	10 US-09-861-289-33	Sequence 33, Appl1
39	34	43.6	11877	9 US-09-860-846-6	Sequence 6, Appl1
40	34	43.6	11877	10 US-09-861-289-6	Sequence 34943, A
41	33	42.3	87	10 US-09-864-761-34943	Sequence 10428, A
42	33	42.3	220	10 US-09-815-242-10428	Sequence 26, Appl1
43	33	42.3	278	9 US-10-027-806-26	Sequence 26, Appl1
44	33	42.3	278	9 US-10-034-623-26	Sequence 26, Appl1
45	33	42.3	292	9 US-09-738-626-5836	Sequence 5836, Ap

## ALIGNMENTS

RESULT 1  
US-09-815-242-10152  
Sequence 10152, Application US/09815242  
Patent No. US2002061569A1  
GENERAL INFORMATION:  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
APPLICANT: Xu, H. Howard  
TITLE OF INVENTION: Identification of Essential Genes in  
FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 10152  
LENGTH: 262  
TYPE: PRT  
ORGANISM: Escherichia coli  
US-09-815-242-10152  
Query Match 62.8%; Score 49; DB 10; Length 262;  
Best Local Similarity 60.0%; Pred. No. 0.17;

Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRYASALGSDGVRV 15  
:|||:|||||  
Db 170 VRYMANAMGPEGVRV 184

## RESULT 2

US-09-815-242-13824  
Sequence 13824, Application US/09815242  
Patent No. US20020061569A1

GENERAL INFORMATION:  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
APPLICANT: Xu, H. Howard  
TITLE OF INVENTION: Identification of Essential Genes in  
Prokaryotes  
FILE REFERENCE: ELITRA.01A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 13824

LENGTH: 269

TYPE: PRT

ORGANISM: Salmonella typhi

US-09-815-242-13824

Query Match 62.8%; Score 49; DB 10; Length 269;  
Best Local Similarity 60.0%; Pred. No. 0.18;

Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRYASALGSDGVRV 15  
:|||:|||||  
Db 177 VRYMANAMGPEGVRV 191

## RESULT 3

US-09-815-242-11851  
Sequence 11851, Application US/09815242  
Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Karl L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

Prokaryotes

FILE REFERENCE: ELITRA.01A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 11851

LENGTH: 265

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-815-242-11851

Query Match 56.4%; Score 44; DB 10; Length 265;  
Best Local Similarity 53.3%; Pred. No. 1.4;

Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRYASALGSDGVRV 15  
:|||:|||||  
Db 173 VRYLAGSLGAEGRV 187

## RESULT 4

US-09-815-242-13289  
Sequence 13289, Application US/09815242  
Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Karl L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

Prokaryotes

FILE REFERENCE: ELITRA.01A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 13289

LENGTH: 315

TYPE: PRT

ORGANISM: Streptococcus pneumoniae

FEATURE:

NAME/KEY: VARIANT

LOCATION: (1)...(315)

OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-815-242-13289

Query Match  
Best Local Similarity 48.7%; Score 38; DB 10; Length 315;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MRYRASALGSDGVRV 15  
|||:|:|:  
DB 281 MMYRAKMGFDATRL 295

RESULT 5  
US-09-738-626-4312

Sequence 4312, Application US/09738626  
Publication No. US20020197605A1

GENERAL INFORMATION:

APPLICANT: NAKAGAWA, SATOSHI  
APPLICANT: MIZOGUCHI, HIROSHI  
APPLICANT: ANDO, SEIKO  
APPLICANT: HAYASHI, MIKIRO  
APPLICANT: OCHIAI, KEIKO  
APPLICANT: YOKOI, HARUHIKO  
APPLICANT: TATEISHI, NAKO  
APPLICANT: SENOH, AKIHIRO  
APPLICANT: IKEDA, MASATO  
APPLICANT: OZAKI, AKIO  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-125

CURRENT APPLICATION NUMBER: US/09/738, 626  
CURRENT FILING DATE: 2000-12-18  
PRIOR APPLICATION NUMBER: JP 99/377484  
PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: JP 00/159162  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: JP 00/280988  
PRIOR FILING DATE: 2000-08-03  
NUMBER OF SEQ ID NOS: 7059  
SOFTWARE: PatentIn ver. 3.0  
SEQ ID NO 4312  
LENGTH: 1233  
TYPE: PRT

ORGANISM: Corynebacterium glutamicum  
US-09-738-626-4312

Query Match  
Best Local Similarity 48.7%; Score 38; DB 9; Length 1233;  
Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 MRYRASALGSDGVRV 16  
::|:|:|:|:  
DB 34 LQARISGIGNDGKIT 49

RESULT 6  
US-09-738-626-4275

Sequence 4275, Application US/09738626  
Publication No. US20020197605A1

GENERAL INFORMATION:

APPLICANT: NAKAGAWA, SATOSHI  
APPLICANT: MIZOGUCHI, HIROSHI  
APPLICANT: ANDO, SEIKO  
APPLICANT: HAYASHI, MIKIRO  
APPLICANT: OCHIAI, KEIKO  
APPLICANT: YOKOI, HARUHIKO  
APPLICANT: TATEISHI, NAKO  
APPLICANT: SENOH, AKIHIRO  
APPLICANT: IKEDA, MASATO  
APPLICANT: OZAKI, AKIO  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-125

CURRENT APPLICATION NUMBER: US/09/738, 626  
CURRENT FILING DATE: 2000-12-18

PRIOR APPLICATION NUMBER: JP 99/377484  
PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: JP 00/159162  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: JP 00/280988  
PRIOR FILING DATE: 2000-08-03  
NUMBER OF SEQ ID NOS: 7059  
SOFTWARE: PatentIn ver. 3.0  
SEQ ID NO 4275  
LENGTH: 441  
TYPE: PRT

ORGANISM: Corynebacterium glutamicum  
US-09-738-626-4275

Query Match  
Best Local Similarity 47.4%; Score 37; DB 9; Length 441;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 ASALGSDGVRV 16  
|:|:|:|:  
DB 146 ATATGPGRLRV 157

RESULT 7  
US-09-738-626-5453

Sequence 5453, Application US/09738626  
Publication No. US20020197605A1

GENERAL INFORMATION:

APPLICANT: NAKAGAWA, SATOSHI  
APPLICANT: MIZOGUCHI, HIROSHI  
APPLICANT: ANDO, SEIKO  
APPLICANT: HAYASHI, MIKIRO  
APPLICANT: OCHIAI, KEIKO  
APPLICANT: YOKOI, HARUHIKO  
APPLICANT: TATEISHI, NAKO  
APPLICANT: SENOH, AKIHIRO  
APPLICANT: IKEDA, MASATO  
APPLICANT: OZAKI, AKIO  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-125

CURRENT APPLICATION NUMBER: US/09/738, 626  
CURRENT FILING DATE: 2000-12-18  
PRIOR APPLICATION NUMBER: JP 99/377484  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: JP 00/159162  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: JP 00/280988  
PRIOR FILING DATE: 2000-08-03  
NUMBER OF SEQ ID NOS: 7059  
SOFTWARE: PatentIn ver. 3.0  
SEQ ID NO 5453  
LENGTH: 722  
TYPE: PRT

ORGANISM: Corynebacterium glutamicum  
US-09-738-626-5453

Query Match  
Best Local Similarity 47.4%; Score 37; DB 9; Length 722;  
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MRYRASALGSDGVR 14  
|||:  
DB 514 MRYAGEQYGSQVR 527

RESULT 8

Sequence 5, Application US/09969362  
Patent No. US20020076790A1

GENERAL INFORMATION:

APPLICANT: Moller, Soren  
APPLICANT: Johansen, Charlotte  
APPLICANT: Schafer, Thomas

APPLICANT: Ostergaard, Peter Rahbek  
APPLICANT: Hoeck, Lisbeth Hedegaard  
TITLE OF INVENTION: A 2,6, -b-D-Fructan Hydrolase Enzyme And  
TITLE OF INVENTION: Process For Using The Enzyme  
FILE REFERENCE: 5540.200-US  
CURRENT APPLICATION NUMBER: US/09/969,362  
CURRENT FILING DATE: 2001-10-02  
PRIOR APPLICATION NUMBER: 09/397,885  
PRIOR FILING DATE: 1999-09-17  
PRIOR APPLICATION NUMBER: PA 1998 01623  
PRIOR FILING DATE: 1998-12-08  
PRIOR APPLICATION NUMBER: 60/101,615  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/111,675  
PRIOR FILING DATE: 1998-12-10  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 5  
LENGTH: 943  
TYPE: PRT  
ORGANISM: Paenibacillus macerans  
US-09-969-362-5

Query Match 47.4%; Score 37; DB 10; Length 943;  
Best Local Similarity 50.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 MRYRSLGSDGV 12  
||| 1:11  
Db 270 LRFRRNGGDTG 281

RESULT 9  
US-10-120-544A-4  
Sequence 4, Application US/10120544A  
Publication No. US20020182693A1  
GENERAL INFORMATION:  
APPLICANT: YOKOYAMA, Masao  
APPLICANT: TANAKA, Masao  
APPLICANT: AYOAGI, Moriochi  
APPLICANT: HASEGAWA, Makoto  
APPLICANT: EHARA, Gaku  
APPLICANT: KIMURA, Masaharu  
APPLICANT: NISHIHASHI, Hideji  
TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or  
TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and  
TITLE OF INVENTION: polynucleotide encoding the same  
FILE REFERENCE: OP1335  
CURRENT APPLICATION NUMBER: US/10/120,544A  
CURRENT FILING DATE: 2002-04-12  
PRIOR APPLICATION NUMBER: JP 2001-115754  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: JP 2001-203463  
PRIOR FILING DATE: 2001-07-04  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 4  
LENGTH: 1316  
TYPE: PRT  
ORGANISM: Bacillus popilliae  
US-10-120-544A-4

Query Match 47.4%; Score 37; DB 9; Length 1316;  
Best Local Similarity 63.6%; Pred. No. 1.6e+02;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 YRASALGSDGV 13  
||| 1:111  
Db 1204 YRQSGYGTG 1214

RESULT 10  
US-10-120-544A-20

Sequence 20, Application US/10120544A  
Publication No. US20020182693A1  
GENERAL INFORMATION:  
APPLICANT: TANAKA, Masao  
APPLICANT: YOKOYAMA, Tomoko  
APPLICANT: AYOAGI, Moriochi  
APPLICANT: HASEGAWA, Makoto  
APPLICANT: EHARA, Gaku  
APPLICANT: KIMURA, Masaharu  
APPLICANT: NISHIHASHI, Hideji  
TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or  
TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and  
TITLE OF INVENTION: polynucleotide encoding the same  
FILE REFERENCE: OP1335  
CURRENT APPLICATION NUMBER: US/10/120,544A  
CURRENT FILING DATE: 2002-04-12  
PRIOR APPLICATION NUMBER: JP 2001-115754  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: JP 2001-203463  
PRIOR FILING DATE: 2001-07-04  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 20  
LENGTH: 1344  
TYPE: PRT  
ORGANISM: Bacillus popilliae  
US-10-120-544A-20

Query Match 47.4%; Score 37; DB 9; Length 1344;  
Best Local Similarity 63.6%; Pred. No. 1.6e+02;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 YRASALGSDGV 13  
||| 1:111  
Db 1208 YRQSGYGTG 1218

RESULT 11  
US-10-120-544A-6  
Sequence 6, Application US/10120544A  
Publication No. US20020182693A1  
GENERAL INFORMATION:  
APPLICANT: TANAKA, Masao  
APPLICANT: YOKOYAMA, Tomoko  
APPLICANT: AYOAGI, Moriochi  
APPLICANT: HASEGAWA, Makoto  
APPLICANT: EHARA, Gaku  
APPLICANT: KIMURA, Masaharu  
APPLICANT: NISHIHASHI, Hideji  
TITLE OF INVENTION: Polypeptide having larvae growth inhibiting or  
TITLE OF INVENTION: insecticidal effect on scarabaeidae insects and  
TITLE OF INVENTION: polynucleotide encoding the same  
FILE REFERENCE: OP1335  
CURRENT APPLICATION NUMBER: US/10/120,544A  
CURRENT FILING DATE: 2002-04-12  
PRIOR APPLICATION NUMBER: JP 2001-115754  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: JP 2001-203463  
PRIOR FILING DATE: 2001-07-04  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 6  
LENGTH: 1386  
TYPE: PRT  
ORGANISM: Bacillus popilliae  
US-10-120-544A-6

Query Match 47.4%; Score 37; DB 9; Length 1386;  
Best Local Similarity 63.6%; Pred. No. 1.7e+02;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 YRASALGSDGV 13  
||| 1:111

Db 1238 YROSGYGTDCV 1248

## RESULT 12

US-09-864-761-40694

Sequence 40694, Application US/09864761  
Patent No. US20020048763A1

## GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

FILE REFERENCE: Aecmca-X-1

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US/09/864,761

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263,6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1

SEQ ID NO 40694

LENGTH: 50

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO AL13458.11

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.6

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.1

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.8

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.9

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.5

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.1

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.3

OTHER INFORMATION: EST\_HUMAN HIT: BF329911.1, EVALUATE 4.00e-15

US-09-864-761-40694

Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 RYRASALGSDGVRV 15

Db 34 RYRASLASKHISV 47

## RESULT 13

US-09-815-242-11279

Sequence 11279, Application US/09815242  
Patent No. US20020061569A1

## GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Karl L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: ELITRA.011A

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: US/09/815,242

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 11279

LENGTH: 295

TYPE: PRT

ORGANISM: Haemophilus influenzae

US-09-815-242-11279

Query Match 46.2%; Score 36; DB 10; Length 295;

Best Local Similarity 50.0%; Pred. No. 42;

Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 RYRASALGSDGVRV 15

Db 204 RYMAADLGKRGIRV 217

## RESULT 14

US-09-738-626-4829

Sequence 4829, Application US/09738626  
Publication No. US20020197605A1

## GENERAL INFORMATION:

APPLICANT: NAKAGAWA, SATOSHI

APPLICANT: MIZOGUCHI, HIROSHI

APPLICANT: ANDO, SEIKO

APPLICANT: HAYASHI, MIKIO

APPLICANT: OCHIAI, KEIKO

APPLICANT: YOKOI, HARUHIKO

APPLICANT: TATEISHI, NAOKO

APPLICANT: SENOH, AKIHIRO

APPLICANT: IKEDA, MASATO

APPLICANT: OZAKI, AKIO

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-125

CURRENT APPLICATION NUMBER: US/09/738,626  
PRIOR FILING DATE: 2000-12-18  
PRIOR APPLICATION NUMBER: JP 99/377484  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: JP 00/159162  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: JP 00/280988  
PRIOR FILING DATE: 2000-08-03  
NUMBER OF SEQ ID NOS: 7059  
SOFTWARE: PatentIn ver. 3.0  
SEQ ID NO 4829  
LENGTH: 358  
TYPE: PRT  
ORGANISM: Corynebacterium glutamicum  
US-09-738-626-4829

Query Match 46.2%; Score 36; DB 9; Length 358;  
Best Local Similarity 50.0%; Pred. No. 52;  
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 YRASALGSDGVRYT 16  
11:1 11:1  
Db 228 YRSSGKGQGVNTT 241

RESULT 15  
US-10-028-072-234  
Sequence 234, Application US/10028072  
Publication No. US2003004311A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang  
TITLE OF INVENTION:  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/028,072  
CURRENT FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 60/049911  
PRIOR FILING DATE: 1997-06-18  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059115  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059117  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059122  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059184  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059352  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059588  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059836  
PRIOR FILING DATE: 1997-09-24

PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062285  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062814  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/062816  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063045  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063082  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/063127  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063327  
PRIOR FILING DATE: 1997-10-27  
PRIOR APPLICATION NUMBER: 60/063329  
PRIOR FILING DATE: 1997-10-27  
PRIOR APPLICATION NUMBER: 60/063550  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063561  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063704  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/063733  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/063735  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/063738  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/063755  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064248  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/064809  
PRIOR FILING DATE: 1997-11-07  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065846  
PRIOR FILING DATE: 1997-11-17  
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;; PRIOR FILING DATE: 1998-05-07  
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;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088741  
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;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/089532  
;; PRIOR FILING DATE: 1998-06-17  
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;; PRIOR APPLICATION NUMBER: 60/089907  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/089947  
;; PRIOR FILING DATE: 1998-06-19  
;; PRIOR APPLICATION NUMBER: 60/090349  
;; PRIOR FILING DATE: 1998-06-23  
;; PRIOR APPLICATION NUMBER: 60/090429  
;; PRIOR FILING DATE: 1998-06-24  
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;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090538  
;; PRIOR FILING DATE: 1998-06-24

;; PRIOR APPLICATION NUMBER: 60/090863  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07

Query Match 46.2%; Score 36; DB 9; Length 1160;  
Best Local Similarity 77.8%; Pred. No. 2e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 4 RASALGSDG 12  
DB 564 RAGALGADG 572

Search completed: January 16, 2003, 10:16:53  
Job time : 12 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 16, 2003, 10:11:12 : Search time 16 Seconds  
(without alignments)  
96.134 Million cell updates/sec

Title: US-09-893-371-2

Sequence: 1 MRYRASALGSDCVAVT 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	62.8	262	1 S48029	enoyl-[acyl-carrie
2	49	62.8	262	1 B43729	enoyl-[acyl-carrie
3	49	62.8	262	2 E90861	enoyl-[acyl-carrie
4	49	62.8	262	2 H85757	enoyl-[acyl-carrie
5	49	62.8	262	2 AD0656	enoyl-[acyl-carrie
6	48	61.5	99	2 S71883	enoyl-[acyl-carrie
7	45	57.7	260	2 G84960	enoyl-[acyl-carrie
8	44	56.4	264	2 AG2354	enoyl-[acyl-carrie
9	44	56.4	265	2 C83419	NADH-dependent eno
10	44	56.4	1112	2 S28289	hypothetical prote
11	44	56.4	1385	2 A88554	protein C38C10.5b
12	44	56.4	1391	2 B88554	protein C38C10.5b
13	42	53.8	291	2 F86451	protein F6N18.2 [i
14	41	52.6	258	2 D95284	probable [imported
15	41	52.6	355	2 T04655	probable serine/th
16	41	52.6	415	2 C85420	protein kinase-lik
17	41	52.6	547	2 A32803	glucan 1,4-alpha-m
18	41	52.6	572	2 T31218	hypothetical prote
19	39	50.0	261	2 C81211	enoyl-[acyl-carrie
20	39	50.0	261	2 E81787	enoyl-[acyl-carrie
21	39	50.0	262	2 AB1196	enoyl-[acyl-carrie
22	39	50.0	262	2 AH1553	enoyl-acyl-carrie
23	39	50.0	274	2 AB2293	hypothetical prote
24	39	50.0	924	2 S75284	chemotaxis protein
25	39	50.0	1296	2 C82521	hemolysin-type cal
26	38.5	49.4	513	2 A90681	probable sensor hi
27	38.5	49.4	513	2 E85531	probable sensor hi
28	38	48.7	109	2 T02716	acidic ribosomal p
29	38	48.7	146	2 T02395	hypothetical prote

30	38	48.7	155	2 H69285	adenylsulfate 3-
31	38	48.7	272	2 E97451	hypothetical prote
32	38	48.7	272	2 AG2669	enoyl-[acyl-carrie
33	38	48.7	312	2 F93164	Hpr(Ser) Kinase/ph
34	38	48.7	316	2 E98030	Hpr(Ser-P) Kinase/p
35	38	48.7	374	2 D86965	probable glycosylt
36	38	48.7	378	1 A70571	probable hexosylar
37	38	48.7	416	2 D71297	probable flagellar
38	38	48.7	424	2 E81358	glutamate-1-semial
39	38	48.7	437	2 B49933	hnsa export system
40	38	48.7	452	2 AC2718	conserved hypotet
41	38	48.7	474	1 BVBRC2	cyae protein - Bor
42	38	48.7	492	2 G97499	probable periplasm
43	38	48.7	513	2 F70776	hypothetical prote
44	38	48.7	545	1 S44486	indole-3-pyruvate
45	38	48.7	547	2 C84593	probable sugar tra

## ALIGNMENTS

RESULT 1  
S48029  
enoyl-[acyl-carrier-protein] reductase (NADH2) (EC 1.3.1.9) - Escherichia coli (strai  
N:Alternate names: enoyl-ACP reductase; short-chain alcohol dehydrogenase homolog env  
C:Species: Escherichia coli  
C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 03-Jun-2002  
C:Accession: S48029; A47681; C64877  
R:Kater, M.M.; Koningsstein, G.M.; Nijkamp, H.J.J.; Stultje, A.R.  
Plant Mol. Biol. 25, 771-790, 1994  
A:Title: The use of a hybrid genetic system to study the functional relationship betw  
A:Reference number: S48029; M0ID:94355651; PMID:8075395  
A:Accession: S48029  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-262 <KAT>  
A:Cross-references: EMBL:X78733; NID:9587105; PIDN:CA55381.1; PID:9587106  
A:Experimental source: strain K-12, substrain W3110  
R:Bergler, H.; Hogenauer, G.; Turnowsky, F.  
J. Gen. Microbiol. 138, 2093-2100, 1992  
A:Title: Sequences of the envM gene and of two mutated alleles in Escherichia coli.  
A:Reference number: A47681; M0ID:93123967; PMID:1364817  
A:Accession: A47681  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-262 <BBP>  
A:Cross-references: GB:M97219; NID:9145850; PIDN:AA17755.1; PID:9145851  
A:Note: sequence extracted from NCBI backbone (NCBIN:121825, NCBI:121826)  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;  
A.: Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; M0ID:97426617; PMID:9278503  
A:Accession: C64877  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-262 <BAT>  
A:Cross-references: GB:AE000227; GB:U00096; NID:91787543; PIDN:AC74370.1; PID:917875  
A:Experimental source: strain K-12, substrain MG1655  
C:Genetics:  
A:Gene: fabI; envM  
C:Function:  
A:Description: catalyzes reduction by NADH of enoyl-acyl-carrier-protein to the corre  
A:Pathway: fatty acid biosynthesis  
A:Note: Inhibited by palmitoyl-CoA and diazaborine  
C:Superfamily: enoyl-[acyl-carrier-protein] reductase (NADH); short-chain alcohol deh  
F:7-190/Domain: fatty acid biosynthesis; homotetramer; inner membrane; NAD; oxidoreductas  
F:9-35/Region: NAD binding

Query Match 62.8%; Score 49; DB 1; Length 262;  
Best Local Similarity 60.0%; Pred. No. 0.44;  
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;



C:Accession: 571883  
C:Perito, B.; Allocat, N.; Casalone, E.; Masulli, M.; Dragani, B.; Polistrelli, M.; Acet  
Biochem. J. 318, 157-162, 1996  
A:Title: Molecular cloning and overexpression of a glutathione transferase gene from *P*  
A:Reference number: 571882; MUID:96358500; PMID:8761466  
A:Accession: 571883  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-99 <P>  
A:Cross-references: EMBL:U38482; NID:g1053074; PIDN:AAC44361.1; PID:g1053075  
A:Experimental source: strain AP 2924  
A:Function:  
A:Description: catalyzes reduction by NADH of enoyl-acyl-carrier-protein to the correspo  
A:Pathway: fatty acid biosynthesis  
C:Superfamily: enoyl-[acyl-carrier-protein] reductase (NADH); short-chain alcohol dehydr  
C:Keywords: fatty acid biosynthesis; inner membrane; NAD; oxidoreductase

Query Match  
Best Local Similarity 61.5%; Score 48; DB 2; Length 99;  
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 MRYRASALGSDGVRY 15  
DB 7 VRYMANMAGEGIRY 21

RESULT 7  
G84960  
enoyl-[acyl-carrier-protein] reductase (NADH2) (EC 1.3.1.9) [imported] - Buchnera sp. (S  
C:Species: Buchnera sp  
C:Date: 02-Mar-2001 #sequence-revision 02-Mar-2001 #text-change 03-Jun-2002  
C:Accession: G84960  
R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.  
Nature 407, 81-86, 2000  
A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A  
A:Reference number: A84930; MUID:20445173; PMID:10993077  
A:Accession: G84960  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-260 <ST>  
A:Cross-references: GB:AP000398; GSPDB:GN00144  
A:Experimental source: strain APS  
C:Genetics:  
A:Gene: fabI; BU265  
C:Superfamily: enoyl-[acyl-carrier-protein] reductase (NADH); short-chain alcohol dehydr  
C:Keywords: oxidoreductase

Query Match  
Best Local Similarity 57.7%; Score 45; DB 2; Length 260;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MRYRASALGSDGVRY 15  
DB 170 VRYMSSLGKEMIRY 184

RESULT 8  
AG2354  
enoyl-[acyl-carrier-protein] reductase [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp.  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence-revision 14-Dec-2001 #text-change 30-Jun-2002  
C:Accession: AG2354  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kunitz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi  
Nakazaki, N.; Shimizu, Y.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AG2354  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-264 <KUR>  
A:Cross-references: GB:BA000019; PIDN:BA876090.1; PID:g17133527; GSPDB:GN00179

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A:Experimental source: strain PCC 7120
C:Genetics:
C:Gene: aII4391
C:Superfamily: enoyl-[acyl-carrier-protein] reductase (NADH); short-chain alcohol dehydrogenase
Query Match 56.4%; Score 44; DB 2; Length 264;
Best Local Similarity 60.0%; Pred. No. 3.5;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 MRRRASALGSDGVRV 15
      ::|||::|||
Db 178 VRYLASLGSGQNTRV 192

RESULT 9
C83419
NADH-dependent enoyl-ACP reductase PA1806 [Imported] - Pseudomonas aeruginosa (strain C)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C83419
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Adam, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapid, K.; Lacey, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; PMID:20437337; PMID:10984043
A:Accession: C83419
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-265 <STO>
A:Cross-references: GB:AE004607; GB:AE004091; NID:g9947789; PIDN:AA05195.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: fabI; PA1806
C:Superfamily: enoyl-[acyl-carrier-protein] reductase (NADH); short-chain alcohol dehydrogenase
Query Match 56.4%; Score 44; DB 2; Length 265;
Best Local Similarity 53.3%; Pred. No. 3.5;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 MRRRASALGSDGVRV 15
      ::|||::|||
Db 173 VRYLASLGAEETRV 187

RESULT 10
S28289
Hypothetical protein C38C10.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 21-Jan-2000
C:Accession: S28289
R:Thomas, K.
submitted to the EMBL Data Library, December 1992
A:Reference number: S28285
A:Accession: S28289
A:Molecule type: DNA
A:Residues: 1-1112 <THO>
A:Cross-references: EMBL:Z19153
C:Genetics:
C:Insertions: 412/1; 612/2; 670/3; 729/3; 914/2; 984/1
C:Superfamily: Caenorhabditis elegans hypothetical protein C38C10.5
Query Match 56.4%; Score 44; DB 2; Length 1112;
Best Local Similarity 50.0%; Pred. No. 16;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 MRRRASALGSDGVRV 16
      ::|||::|||
Db 1040 IRRRASQMGDGVNAT 1055

RESULT 11
A88354

```

